



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 130245

TO: Jeffrey Parkin
Location: REM-3D39/3E18
Art Unit: 1648
Thursday, September 02, 2004

Case Serial Number: 10/001407

From: Toby Port
Location: Biotech-Chem Library
Remsen 1A59
Phone: 571-272-2523

toby.port@uspto.gov

Search Notes

Dear Examiner Parkin,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port

THIS PAGE BLANK (CONT.)

From: Parkin, Jeffrey
 Sent: Wednesday, August 18, 2004 10:16 PM
 To: STIC-Biotech/ChemLib
 Subject: Sequence Search: U.S. Serial No. 10/001,407

Please search **SEQ ID NOS.: 10 and 15** from **U.S. Serial No. 10/001,407** (Yang, Y., and T. Burrell) v. all relevant databases, including interference. SEQ ID NO.: 10 corresponds to a region of the HIV-2 genome so it will probably pick up a large number of full-length sequences. **Can you limit the search results to pick up ONLY nucleic acid sequences that are =<100 nucleotides in length for both sequences?**

Place results on both disk and paper.

Thanks!

JSP
 REM 3D39
 AU 1648
 2-0908

STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-_____
 Date Searcher Picked up: _____
 Date Completed: _____
 Searcher Prep/Rev. Time: _____
 Online Time: _____

Type of Search

NA Sequence: # _____
 AA Sequence :# _____
 Structure: # _____
 Bibliographic: _____
 Litigation: _____
 Patent Family: _____
 Other: _____

Vendors and cost where applicable

STN: _____
 DIALOG: _____
 QUESTEL/ORBIT: _____
 LEXIS/NEXIS: _____
 SEQUENCE SYSTEM: _____
 WWW/Internet: _____
 Other(Specify): _____

THIS PAGE BLANK (USPTO)

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:20:52 ; Search time 526.623 Seconds

(without alignments)
2057.592 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 cggcgcccaaccctcctagggatttc 25

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1846492

Minimum DB seq length: 0
Maximum DB seq length: 100Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

```
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_ov:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*
```

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	6	AX498422 Sequence
2	25	100.0	34	6	AX498420 Sequence
3	25	100.0	34	6	AX498421 Sequence
4	25	100.0	52	6	AX498427 Sequence
5	19	76.0	88	14	HIVTRAJ
6	18	72.0	25	6	AX498426 Sequence
7	18	72.0	58	6	AX498431 Sequence
8	17	68.0	22	6	AR093423 Sequence
9	17	68.0	22	6	E30948
10	16.6	66.4	24	6	AX498425 Sequence
11	16.6	66.4	32	6	BD161898
12	16.6	66.4	42	6	AR011291
13	16.6	66.4	42	6	I17929
14	16.6	66.4	57	6	AX498430 Sequence
15	16.2	64.8	100	6	AX112460 Sequence
16	16.2	64.8	100	6	AX112461 Sequence
17	16	64.0	90	14	HIVTRAAB
18	16	64.0	90	14	HIVTRAAC
19	16	64.0	90	14	HIVTRAAD
20	16	64.0	90	14	HIVTRADE
21	16	64.0	90	14	HIVTRAEE
22	16	64.0	90	14	HIVTRAFF
23	16	64.0	90	14	HIVTRAG
24	16	64.0	90	14	HIVTRAHH
25	15.4	61.6	33	6	AR410466 Sequence
26	15.4	61.6	33	6	AX317289 Sequence
27	15.4	61.6	37	6	BD268930 Anti-Vira
28	15.4	61.6	37	6	AR302583 Sequence
29	15.4	61.6	37	6	AX019151 Sequence
30	15.4	61.6	37	6	AX035482 Sequence
31	15.4	61.6	37	6	AX056855 Sequence
32	15.4	61.6	37	6	BD130487 Antiviral
33	15.2	60.8	95	6	AX119975 Sequence
34	15.2	60.8	95	6	AX138024 Sequence
35	15	60.0	81	14	AF040785 Hepatitis
36	15	60.0	81	14	AF040804 Hepatitis
37	15	60.0	81	14	AF040854 Hepatitis
38	15	60.0	89	14	HIVTRAII
39	15	60.0	89	14	HIVTRAJJ
40	14.8	59.2	20	6	AX119964 Sequence
41	14.8	59.2	20	6	AX138017 Sequence
42	14.4	57.6	50	9	AY102626 Homo sapi
43	14.4	57.6	52	6	AX347672 Sequence
44	14.4	57.6	70	6	E33310 DbpA/DbpB/D
45	14.4	57.6	99	14	S63302 vpu-membran

ALIGNMENTS

RESULT 1
AX498422 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 10 from Patent WO0234951.
ACCESSION AX498422
VERSION AX498422.1 GI:23343300
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORANISM Human immunodeficiency virus 2
Lentivirus group.
REFERENCE
1 Yang Y.Y. and Burrell T.A.
AUTHORS Compositions and methods for detecting human immunodeficiency virus
TITLE 2 (hiv-2)

JOURNAL Patent: WO 0234951-A 10 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
Source 1..25
/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.87;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCACCTGCTAGGATTTT 25
1 CGGGCGCCACCTGCTAGGATTTT 25
Db 1 CGGGCGCCACCTGCTAGGATTTT 25

RESULT 2
AX498420/c 34 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 8 from Patent WO0234951.
DEFINITION AX498420
ACCESSION AX498420
VERSION AX498420.1 GI:23343298
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORGANISM Human immunodeficiency virus 2
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 Yang, Y.Y. and Burrell, T.A.
AUTHORS 2 (HIV-2)
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 8 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
Source 1..34
/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCACCTGCTAGGATTTT 25
25 CGGGCGCCACCTGCTAGGATTTT 1
Db 25 CGGGCGCCACCTGCTAGGATTTT 1

RESULT 3
AX498421 34 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 9 from Patent WO0234951.
DEFINITION AX498421
ACCESSION AX498421
VERSION AX498421.1 GI:23343299
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORGANISM Human immunodeficiency virus 2
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 Yang, Y.Y. and Burrell, T.A.
AUTHORS 2 (HIV-2)
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 9 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
Source 1..34
/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCACCTGCTAGGATTTT 25
10 CGGGCGCCACCTGCTAGGATTTT 34
Db 10 CGGGCGCCACCTGCTAGGATTTT 34

RESULT 4
AX498427 52 bp DNA linear PAT 26-SEP-2002
LOCUS Sequence 15 from Patent WO0234951.
DEFINITION AX498427
ACCESSION AX498427
VERSION AX498427.1 GI:23343305
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
ARTIFICIAL SEQUENCES.
REFERENCE 1 Yang, Y.Y. and Burrell, T.A.
AUTHORS 2 (HIV-2)
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 15 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
Source 1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"

ORIGIN
Query Match 100.0%; Score 25; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCACCTGCTAGGATTTT 25
28 CGGGCGCCACCTGCTAGGATTTT 52
Db 28 CGGGCGCCACCTGCTAGGATTTT 52

RESULT 5
HIV1TRAJ 88 bp DNA linear VRL 02-AUG-1993
LOCUS Human immunodeficiency virus type 2 long terminal repeat region,
DEFINITION partial sequence, clone 1.
ACCESSION M74763
VERSION M74763.1 GI:327981
KEYWORDS long terminal repeat (LTR).
SOURCE Human immunodeficiency virus 2
ORGANISM Human immunodeficiency virus 2
VIRUSES; Retroviral viruses; Retroviridae; Lentivirus; Primate
lentivirus group.
REFERENCE 1 Whitcomb, J.M. and Hughes, S.H.
AUTHORS 1 (bases 1 to 88)
TITLE The sequence of human immunodeficiency virus type 2 circle junction
suggests that integration protein cleaves the ends of linear DNA
asymmetrically
JOURNAL J. Virol. 65 (7), 3906-3910 (1991)
MEDLINE 91251249
PUBMED 2041100
COMMENT Original source text: Human immunodeficiency virus type 2 DNA.
FEATURES Location/Qualifiers
Source 1..88
/organism="Human immunodeficiency virus 2"
/proviral
/mol_type="genomic DNA"
/db_xref="taxon:11709"

LTR 1. .88

ORIGIN

Query Match 76.0%; Score 19; DB 14; Length 88;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 CCAACCTGCTAGGATTTT 25
|||||
Db 48 CCAACCTGCTAGGATTTT 30

RESULT 6
AX498426
LOCUS AX498426 25 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 14 from Patent WO0234951.
ACCESSION AX498426
VERSION AX498426.1 GI:23343304
KEYWORDS
SOURCE Human immunodeficiency virus 2 (HIV-2)
ORGANISM Human immunodeficiency virus 2
VIRUSES; Retroviridae; Lentivirus; Primate
Lentivirus group.

REFERENCE
AUTHORS Yang, Y.Y. and Burrell, T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 14 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
source Location/Qualifiers
1. .25
/organism="Human immunodeficiency virus 2"
/mol_type="unassigned DNA"
/db_xref="taxon:11709"

ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCAACTGCTAG 18
|||||
Db 8 CGGGCGCCAACTGCTAG 25

RESULT 7
AX498431
LOCUS AX498431 58 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 19 from Patent WO0234951.
ACCESSION AX498431
VERSION AX498431.1 GI:23343309
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE
AUTHORS Yang, Y.Y. and Burrell, T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 19 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
source Location/Qualifiers
1. .58
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"

ORIGIN

Query Match 72.0%; Score 18; DB 6; Length 58;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCAACTGCTAG 18
|||||
Db 41 CGGGCGCCAACTGCTAG 58

RESULT 8
AR093423
LOCUS AR093423 22 bp DNA linear PAT 08-SEP-2000
DEFINITION Sequence 31 from patent US 6001558.
ACCESSION AR093423
VERSION AR093423.1 GI:10020172
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE
AUTHORS Backus, J.W., Atwood, S.M., Casey, A.E., Rasmussen, E.B. and
Cummins, T.J.
TITLE Amplification and detection of HIV-1 and/or HIV 2
JOURNAL Patent: US 6001558-A 31 14-DEC-1999;
FEATURES
source Location/Qualifiers
1. .22
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 22;
Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGGCGCCAACTGCTA 17
|||||
Db 6 CGGGCGCCAACTGCTA 22

RESULT 9
E30948
LOCUS E30948 22 bp DNA linear PAT 18-JUN-2001
DEFINITION Amplification and detection of HIV-1 and/or HIV-2.
ACCESSION E30948
VERSION E30948.1 GI:13025679
KEYWORDS JP 1999069987-A/31.
SOURCE unidentified
ORGANISM unidentified
unclassified.

REFERENCE
AUTHORS John, W.B., Suzan, M.A., Ann, E.K., Eric, B.R. and Thomas, J.K.
TITLE Amplification and detection of HIV-1 and/or HIV-2
JOURNAL Patent: JP 1999069987-A 31 16-MAR-1999;
ORTHOGONAL DIAGNOSTICS INC
COMMENT OS Unidentified
PN JP 1999069987-A/31
PD 16-MAR-1999
PF 24-JUN-1998 JP 1998177059
PR 25-JUN-1997 US 60/050759
PI JOHN WESLEY BACKUS, SUZAN MERISSA ATWOOD, ANN ELIZABETH KEIJI,
ERIC BRICE RASMUSSEN, THOMAS JOSEPH KAMINDU
PC C12N15/09, C1201/68, G01N33/566, G01N33/569, C12N15/00 CC
Strandedness: Single;
CC Topology: Linear;
FH key Location/Qualifiers
FT source 1. .22
/organism="unidentified".
Location/Qualifiers
1. .22
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

ORIGIN

Query Match 68.0%; Score 17; DB 6; Length 22;

Best Local Similarity 100.0%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGGCGCCACCTGCTA 17
Db 6 CGGCGCCACCTGCTA 22

RESULT 10

AX498425

LOCUS

AX498425 Sequence 13 from Patent WO0234951. 24 bp DNA linear PAT 26-SEP-2002
AX498425
AX498425.1 GI:23343303

SOURCE

synthetic construct
synthetic construct
artificial sequences.

REFERENCE

AUTHORS

Yang, Y. Y. and Burrell, T. A.

JOURNAL

Compositions and methods for detecting human immunodeficiency virus
2 (Hiv-2)
Patent: WO 0234951-A 13 02-MAY-2002;
Gen-Probe Incorporated (US)

FEATURES

Location/Qualifiers
1..24

ORIGIN

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 6; Length 24;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCGCCACCTGCTAGGATTTT 25
Db 2 GGGCGCCACCTGCTAGGATTTT 24

RESULT 11

BD161898

LOCUS

BD161898 Nonhuman primate model of acquired immunodeficiency syndrome. 32 bp DNA linear PAT 17-JAN-2003
BD161898
BD161898.1 GI:27867656

KEYWORDS

UP 2002159296-A/7.

SOURCE

synthetic construct
artificial sequences.

REFERENCE

AUTHORS

Shinohara, K., Sakai, K. and Honda, M.

JOURNAL

Nonhuman primate model of acquired immunodeficiency syndrome
Patent: UP 2002159296-A 7 04-JUN-2002;
DIRECTOR GENERAL OF NATIONAL INSTITUTE OF INFECTIOUS DISEASES, THE
ORGANIZATION FOR PHARMACEUTICAL SAFETY AND RESEARCH

ORIGIN

Location/Qualifiers
1..32

COMMENT

UP 2002159296-A/7
PD 04-JUN-2002 JP 2000360274
PI KATSUBAKI SHINOHARA, KOJI SAKAI, MITSUO HONDA
PC C12N15/09, A01K67/027, C12N7/00, C12N7/02, G01N33/15, G01N33/50//
PC G01N33/569,
PC (C12N7/00, C12R1:93), (C12N7/02, C12R1:93), C12N15/00 CC
Description of Artificial Sequence: artificially synthesized CC
primer

CC

sequence

FH

Key

Location/Qualifiers

FT

source

1..32
/organism='Artificial Sequence',
Location/Qualifiers

source

1..32
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

Query Match 66.4%; Score 16.6; DB 6; Length 32;
Best Local Similarity 82.6%; Pred. No. 9.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 GGGCGCCACCTGCTAGGATTTT 25
Db 1 GGGCGCATTCCTGCTAGGATTTT 23

RESULT 12

AR011291

LOCUS

AR011291 Sequence 160 from patent US 5762938. 42 bp DNA linear PAT 04-DEC-1998
AR011291
AR011291.1 GI:3969281

VERSION

AR011291.1 GI:3969281

KEYWORDS

Unknown.

SOURCE

Unknown.

REFERENCE

AUTHORS

Paoletti, E., Perkus, M. E., Taylor, J., Tartaglia, J., Norton, B. K.,
Riviere, M., de Taisne, C., Limbach, K. J., Johnson, G. P., Pincus, S. E.,
Cox, W. I., Audonnet, J.-C., Francis, and Gettig, R. Robert.
Modified recombinant vaccinia virus and expression vectors thereof
Patent: US 5762938-A 160 09-JUN-1998;

JOURNAL

Location/Qualifiers
1..42

ORIGIN

source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 66.4%; Score 16.6; DB 6; Length 42;
Best Local Similarity 82.6%; Pred. No. 9.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGCGCCACCTGCTAGGATTTT 24
Db 9 GGGCGATCAGCAGCTAGGATTTT 31

RESULT 13

117929

LOCUS

117929 Sequence 160 from patent US 5494807. 42 bp DNA linear PAT 07-OCT-1996
117929
117929.1 GI:1598284

KEYWORDS

Unknown.

SOURCE

Unknown.

REFERENCE

AUTHORS

Paoletti, E., Perkus, M. E., Taylor, J., Tartaglia, J., Norton, B. K.,
Riviere, M., de Taisne, C., Limbach, K. J., Johnson, G. P., Pincus, S. E.,
Cox, W. I., Audonnet, J.-C., Francis, and Gettig, R. R.

JOURNAL

NYVAC vaccine virus recombinants comprising heterologous inserts
Patent: US 5494807-A 160 27-FEB-1996;

FEATURES

Location/Qualifiers
1..42

ORIGIN

source
/organism="unknown"
/mol_type="unassigned DNA"

Query Match 66.4%; Score 16.6; DB 6; Length 42;
Best Local Similarity 82.6%; Pred. No. 9.4e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 2 GGGCGCCACCTGCTAGGATTTT 24

Db 9 GGGCATCAAGAGCTAGGATTT 31

Search completed: August 31, 2004, 02:04:24
job time : 527.623 secs

RESULT 14
AX498430 57 bp DNA linear PAT 26-SEP-2002
LOCUS AX498430
DEFINITION Sequence 18 from Patent WO0234951.
ACCESSION AX498430
VERSION AX498430.1 GI:23343308
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1 Yang, Y.Y. and Burrell, T.A.
AUTHORS Compositions and methods for detecting human immunodeficiency virus
TITLE 2 (hiv-2)
JOURNAL Patent: WO 0234951-A 18 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES
Location/Qualifiers
1..57
source
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of the sequence given as SEQ ID
NO:13"

ORIGIN

Query Match 66.4%; Score 16.6; DB 6; Length 57;
Best Local Similarity 82.6%; Pred. No. 9.1e+03;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 GGGCCCACTGCTAGGATTTT 25
Db 35 GGGCCCACTGCTAGGATTTT 57

RESULT 15
AX112460 100 bp DNA linear PAT 01-MAY-2001
LOCUS AX112460
DEFINITION Sequence 108 from Patent WO0127857.
ACCESSION AX112460
VERSION AX112460.1 GI:13939219
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Braun, A., Koester, H., van den Boom, D., Ping, Y., Rodl, C., He, L.,
AUTHORS Chiu, N. and Jurinke, C.
TITLE Methods for generating databases and databases for identifying
JOURNAL polymorphic genetic markers
Patent: WO 0127857-A 108 19-APR-2001;
Sequenom, Inc. (US)
FEATURES
Location/Qualifiers
1..100
source
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 64.8%; Score 16.2; DB 6; Length 100;
Best Local Similarity 85.7%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGGCCCACTGCTAGGAT 22
Db 64 GGGCCCACTGCTAGGAT 84

THIS PAGE BLANK (USPTO)

CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesize amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 25 BP; 4 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CGGGGCCCACTGCTAGGATTTT 25
1 CGGGGCCCACTGCTAGGATTTT 25

RESULT 2
ABK93885
ID ABK93885 standard; DNA; 34 BP.

AC ABK93885;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus type 2 detection probe #9.

XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
XX hepatitis C virus; HCV; probe; ss.

OS Human immunodeficiency virus 2.

XX WO200234951-A2.

XX 02-MAY-2002.

XX 22-OCT-2001; 2001WO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

PR 30-MAR-2001; 2001US-0280058P.

PA (GENP-) GEN-PROBE INC.

PI Yang YF, Burrell TA;

XX WPI; 2002-489953/52.

PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
XX duplex.

PS Claim 1; Page 22; 58pp; English.

CC The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NA with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detecting the amplified NA; or providing a
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesize amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 34 BP; 4 A; 10 C; 10 G; 10 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CGGGGCCCACTGCTAGGATTTT 25
10 CGGGGCCCACTGCTAGGATTTT 34

RESULT 3
ABK93884/C
ID ABK93884 standard; DNA; 34 BP.

AC ABK93884;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus type 2 detection probe #8.

XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
XX hepatitis C virus; HCV; probe; ss.

OS Human immunodeficiency virus 2.

XX WO200234951-A2.

XX 02-MAY-2002.

XX 22-OCT-2001; 2001WO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

PR 30-MAR-2001; 2001US-0280058P.

PA (GENP-) GEN-PROBE INC.

PI Yang YF, Burrell TA;

XX WPI; 2002-489953/52.

PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
XX duplex.

PS Example 1; Page 39; 58pp; English.

CC The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NA with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detecting the amplified NA; or providing a
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesize amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 34 BP; 10 A; 10 C; 10 G; 4 T; 0 U; 0 Other;

Query Match 100.0%; Score 25; DB 6; Length 34;
Best Local Similarity 100.0%; Pred. No. 0.011;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 CGGGGCCCACTGCTAGGATTTT 25
25 CGGGGCCCACTGCTAGGATTTT 1

```

RESULT 4
ABK93891
ID ABK93891 standard; DNA; 52 BP.
XX
AC ABK93891;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus type 2 detection probe #15.
XX
KM Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
OS Human immunodeficiency virus 2.
XX
PN WO200234951-A2.
XX
PD 02-MAY-2002.
XX
PF 22-OCT-2001; 2001WO-US045396.
XX
PR 23-OCT-2000; 2000US-0242620P.
PR 30-MAR-2001; 2001US-0280058P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Yang YY, Burrell TA;
XX
PS WPI; 2002-489953/52.
XX
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
PT duplex.
XX
PS Claim 11; Page 25; 58pp; English.
XX
CC The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesise amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 25; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCCAACTGCTAGGATTT 25
Db 28 CGGGCGCCCAACTGCTAGGATTT 52

```

```

DE Human immunodeficiency virus type 2 detection probe #14.
XX
KM Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
OS Human immunodeficiency virus 2.
XX
PN WO200234951-A2.
XX
PD 02-MAY-2002.
XX
PF 22-OCT-2001; 2001WO-US045396.
XX
PR 23-OCT-2000; 2000US-0242620P.
PR 30-MAR-2001; 2001US-0280058P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Yang YY, Burrell TA;
XX
PS WPI; 2002-489953/52.
XX
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
PT duplex.
XX
PS Claim 10; Page 25; 58pp; English.
XX
CC The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C
CC and D of HIV-2. The method is useful for amplifying and detecting the NA
CC in blood serum and also as components of multiplex amplification
CC reactions that synthesise amplicons corresponding to polynucleotides of
CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
CC virus (HCV). ABK93877-ABK93910 represent HIV-2 detection probes of the
CC invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 25 BP; 3 A; 10 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 72.0%; Score 18; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCCCAACTGCTAG 18
Db 8 CGGGCGCCCAACTGCTAG 25

```

```

RESULT 5
ABK93890
ID ABK93890 standard; DNA; 25 BP.
XX
AC ABK93890;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX

```

```

RESULT 6
ABK93895
ID ABK93895 standard; DNA; 58 BP.
XX
AC ABK93895;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus type 2 detection probe #19.
XX
KM Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
OS Human immunodeficiency virus 2.
XX
PN WO200234951-A2.
XX

```

PD 02-MAY-2002.

XX 22-OCT-2001; 2001WO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

XX 30-MAR-2001; 2001US-0280058P.

XX (GENP-) GEN-PROBE INC.

XX Yang YY, Burrell TA;

XX WPI; 2002-48953/52.

XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by

XX acid, or hybridizing nucleic acid with a probe and detecting probe:target

XX duplex.

XX Claim 11; Page 25; 58pp; English.

XX The invention relates to a method of detecting human immunodeficiency

XX virus-2 nucleic acids (NA) in a biological sample, by contacting NA with

XX base sequence, and detecting the amplified NA; or providing a

XX hybridization probe and detecting the amplified NA; or providing a

XX probe to form probe:target duplex, and detecting the duplex. The method

XX is useful for detecting the presence of HIV-2 NA in a lysate or a blood

XX product such as plasma or serum, and also for detecting subtypes A, B, C

XX in blood serum and also as components of multiplex amplification

XX reactions that synthesize amplicons corresponding to polynucleotide

XX unrelated viruses, e.g., HIV-1, hepatitis B virus (HBV) and hepatitis C

XX virus (HCV). ABR9387-ABK93910 represent HIV-2 detection probes of the

XX invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 58 BP; 17 A; 17 C; 13 G; 11 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 72.0%; Score 18; DB 6; Length 58;

XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 CGGGCGCCCAACTGCTAG 18

XX 41 CGGGCGCCCAACTGCTAG 58

XX RESULT 7

XX AAV63697

XX ID AAV63697 standard; DNA; 22 BP.

XX AAV63697;

XX 11-MAR-1999 (first entry)

XX PCR primer used to amplify HIV-2 sequences.

XX HIV-1; HIV-2; detection; Acquired Immunodeficiency Syndrome; AIDS;

XX co-amplification assay; PCR primer; ss.

XX Synthetic.

XX Human immunodeficiency virus 2.

XX EP887427-A2.

XX 30-DEC-1998.

XX 24-JUN-1998; 98BP-00304959.

XX 25-JUN-1997; 97US-0050759P.

XX (ORTH-) ORTHO-CLINICAL DIAGNOSTICS INC.

XX Beckus JW, Atwood SM, Casey AE, Rasmussen EB, Cummins TJ;

XX WPI; 1999-047891/05.

XX Detecting Human Immunodeficiency Virus 1 and 2 - using at least four new

XX oligonucleotide primers and multiple detection probes.

XX Disclosure; Page 11; 25pp; English.

XX The present PCR primer is used to amplify human deficiency type 2 (HIV-2)

XX nucleic acids. The specification also describes primers and probes for

XX HIV-1 and HIV-2. The primers and probes are useful for amplifying and

XX detecting HIV-1 and HIV-2 and all their subtype nucleic acids in

XX biological samples; and for giving progress in our understanding of

XX Acquired Immunodeficiency Syndrome (AIDS). The primers are able to detect

XX all HIV-1 and HIV-2 subtypes without detecting non-related viruses. The

XX primer sets for HIV-1 and HIV-2 are compatible with each other, and can

XX be combined to form a co-amplification assay for HIV-1 and HIV-2. Using

XX more than one primer set to amplify target nucleic acid sequences which

XX overlap a common probe region maximises strain sensitivity and robustness

XX Sequence 22 BP; 3 A; 8 C; 6 G; 5 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 68.0%; Score 17; DB 2; Length 22;

XX Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX Db 1 CGGGCGCCCAACTGCTA 17

XX 6 CGGGCGCCCAACTGCTA 22

XX RESULT 8

XX ABR93889

XX ID ABR93889 standard; DNA; 24 BP.

XX ABR93889;

XX 29-AUG-2003 (revised)

XX 26-AUG-2002 (first entry)

XX Human immunodeficiency virus type 2 detection probe #13.

XX Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;

XX hepatitis C virus; HCV; probe; ss.

XX Human immunodeficiency virus 2.

XX WO200234951-A2.

XX 02-MAY-2002.

XX 22-OCT-2001; 2001WO-US045396.

XX 23-OCT-2000; 2000US-0242620P.

XX 30-MAR-2001; 2001US-0280058P.

XX (GENP-) GEN-PROBE INC.

XX Yang YY, Burrell TA;

XX WPI; 2002-48953/52.

XX Detecting human immunodeficiency virus-2 nucleic acids in a sample, by

XX acid, or hybridizing nucleic acid with a probe and detecting probe:target

XX duplex.

XX Claim 10; Page 25; 58pp; English.

XX The invention relates to a method of detecting human immunodeficiency

XX virus-2 nucleic acids (NA) in a biological sample, by contacting NA with

XX base sequence, and detecting the amplified NA; or providing a

CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
 CC probe to form probe:target duplex, and detecting the duplex. The method
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
 CC product such as plasma or serum, and also for detecting subtypes A, B, C
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC in blood serum and also as components of multiplex amplification
 CC reactions that synthesise amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABR93877-ABK93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 24 BP; 3 A; 7 C; 8 G; 6 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 6; Length 24;

Best Local Similarity 82.6%; Pred. No. 1.8e+02; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3 GGGCCCAACCTGCTAGGATTTT 25
 ||| |||||
 2 GGGGCCACCTGCTAGGATTTT 24

AAQ35348 standard; DNA; 42 BP.

25-MAR-2003 (revised)

18-MAY-1993 (first entry)

MUNSVISR, a mutagenesis primer for env gene.

Human immunodeficiency virus; HIV; amplification; ss.

Synthetic.

WO9222641-A1.

23-DEC-1992.

12-JUN-1992; 92WO-US005107.

14-JUN-1991; 91US-00715921.

11-JUN-1992; 92US-00897382.

(VIRO-) VIROGENETICS CORP.

Paolotti E, Tartaglia J, Cox WJ;

WPI; 1993-018128/02.

Modified recombinant virus with inactivated non-essential genetic

functions - comprises e.g. vaccinia or avipox virus, used as HIV vaccine.

Example 3; Page 49; 159pp; English.

The env gene of HIV was subjected to in vitro mutagenesis to remove the
 CC sequences encoding the rex protein and the LTR region from the 3' end of
 CC the gene and to delete the putative immuno-suppressive (IS) region (amino
 CC acids 583-599). Mutagenesis was performed using primers LTR2 and
 CC MUNSISR using PIR25mutenv8 as template. Mutagenised clones were
 CC identified by hybridisation and restriction analysis. See also AAQ35328-
 CC 437. (Updated on 25-MAR-2003 to correct PN field.)

Sequence 42 BP; 8 A; 8 C; 15 G; 11 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 2; Length 42;

Best Local Similarity 82.6%; Pred. No. 2e+02; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2 GGGCCCAACCTGCTAGGATTTT 24
 ||| |||||

Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 10

ID ABR93894 standard; DNA; 57 BP.

ABR93894;

29-AUG-2003 (revised)

26-AUG-2002 (first entry)

Human immunodeficiency virus type 2 detection probe #18.

Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;

hepatitis C virus; HCV; probe; ss.

Human immunodeficiency virus 2.

WO200234951-A2.

22-OCT-2001; 2001WO-US045396.

23-OCT-2000; 2000US-0242620P.

30-MAR-2001; 2001US-0280058P.

(GENP-) GEN-PROBE INC.

Yang YY, Burrell TA;

WPI; 2002-489953/52.

Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
 PT duplex.

Claim 11; Page 25; 58pp; English.

The invention relates to a method of detecting human immunodeficiency
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
 CC base sequence, and detecting the amplified NA, or providing a
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
 CC probe to form probe:target duplex, and detecting the duplex. The method
 CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
 CC product such as plasma or serum, and also for detecting subtypes A, B, C
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC in blood serum and also as components of multiplex amplification
 CC reactions that synthesise amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABR93877-ABK93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

Sequence 57 BP; 17 A; 14 C; 14 G; 12 T; 0 U; 0 Other;

Query Match 66.4%; Score 16.6; DB 6; Length 57;

Best Local Similarity 82.6%; Pred. No. 2.1e+02; Indels 0; Gaps 0;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

3 GGGCCCAACCTGCTAGGATTTT 25
 ||| |||||

35 GGGGCCACCTGCTAGGATTTT 57

RESULT 11

AAH02411 standard; DNA; 100 BP.

AAH02411;

DT 12-JUN-2001 (first entry)
 DE Human Factor XIII coding sequence fragment SEQ ID NO: 108.
 XX
 XX Database; polymorphism; SNP; human; genetic marker; disease; infection;
 KM drug response; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200127857-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028413.
 XX
 PR 13-OCT-1999; 99US-0159176P.
 XX
 PR 10-JUL-2000; 2000US-0217251P.
 XX
 PR 10-JUL-2000; 2000US-0217658P.
 XX
 PR 19-SEP-2000; 2000US-00663968.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Braun A, Koester H, Van Den Boom D, Ping Y, Rodi C, He L,
 PI Chiu N, Jurinke C;
 XX
 DR WPI; 2001-273865/28.
 XX
 PT Producing a database for identifying polymorphic genetic markers,
 PT comprises obtaining data relating to members of a healthy population and
 PT entering the information into a database.
 XX
 PS Example 9; Page 303; 304pp; English.
 XX
 CC The present invention provides a database of human samples obtained from
 CC healthy individuals which can be used to identify polymorphic genetic
 CC markers. Data obtained for the database can be used to sort the samples
 CC by parameters such as age, sex and ethnicity. This is useful in linking
 CC markers with diseases, susceptibility to infection and drug responses.
 CC The present sequence was used in an assay to demonstrate the uses of the
 CC database of the invention
 XX
 SQ Sequence 100 BP; 23 A; 31 C; 28 G; 18 T; 0 U; 0 Other;
 XX
 QY Query Match 64.8%; Score 16.2; DB 4; Length 100;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 2 GGGCGCAACCTGCTAGGAT 22
 64 GGGCGTCAACCTGCAAGTAT 84
 RESULT 12
 ID AAH02412 standard; DNA; 100 BP.
 XX
 AC AAH02412;
 XX
 DT 12-JUN-2001 (first entry)
 XX
 DE Human Factor XIII coding sequence fragment SEQ ID NO: 109.
 XX
 DE Database; polymorphism; SNP; human; genetic marker; disease; infection;
 KM drug response; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200127857-A2.
 XX
 PD 19-APR-2001.
 XX
 PF 13-OCT-2000; 2000WO-US028413.
 XX

PR 13-OCT-1999; 99US-0159176P.
 PR 10-JUL-2000; 2000US-0217251P.
 PR 10-JUL-2000; 2000US-0217658P.
 PR 19-SEP-2000; 2000US-00663968.
 XX
 PA (SEQU-) SEQUENOM INC.
 XX
 PI Braun A, Koester H, Van Den Boom D, Ping Y, Rodi C, He L,
 PI Chiu N, Jurinke C;
 XX
 DR WPI; 2001-273865/28.
 XX
 PT Producing a database for identifying polymorphic genetic markers,
 PT comprises obtaining data relating to members of a healthy population and
 PT entering the information into a database.
 XX
 PS Example 9; Page 303; 304pp; English.
 XX
 CC The present invention provides a database of human samples obtained from
 CC healthy individuals which can be used to identify polymorphic genetic
 CC markers. Data obtained for the database can be used to sort the samples
 CC by parameters such as age, sex and ethnicity. This is useful in linking
 CC markers with diseases, susceptibility to infection and drug responses.
 CC The present sequence was used in an assay to demonstrate the uses of the
 CC database of the invention
 XX
 SQ Sequence 100 BP; 23 A; 31 C; 27 G; 19 T; 0 U; 0 Other;
 XX
 QY Query Match 64.8%; Score 16.2; DB 4; Length 100;
 Best Local Similarity 85.7%; Pred. No. 3.7e+02;
 Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 DB 2 GGGCGCAACCTGCTAGGAT 22
 64 GGGCGTCAACCTGCAAGTAT 84
 RESULT 13
 ID ACC00078 standard; DNA; 33 BP.
 XX
 AC ACC00078;
 XX
 DT 26-JUN-2003 (first entry)
 XX
 DE Primer #4 related to human retinoblastoma binding protein.
 XX
 DE Human; retinoblastoma binding protein 34.54; tumour; ss; primer.
 XX
 OS Homo sapiens.
 XX
 PN CN1380303-A.
 XX
 PD 20-NOV-2002.
 XX
 PF 11-APR-2001; 2000CN-00125808.
 XX
 PR 11-APR-2001; 2000CN-00125808.
 XX
 PR (SHAN-) SHANGHAI BOWINDOM GENE DEV INC.
 XX
 PI Mao Y, Xie Y;
 XX
 DR WPI; 2003-222536/22.
 XX
 A novel polypeptide-human retinoblastoma binding protein 34.54.
 XX
 PS Example 4; Page 21; 35pp; Chinese.
 XX
 CC The present invention relates to human retinoblastoma binding protein
 CC 34.54, used to treat various tumours. The present sequence represents a
 CC primer related to human retinoblastoma binding protein encoding sequence

THIS PAGE BLANK (3870)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:14:18 / Search time 1266.56 Seconds

(without alignments)
589.436 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 cggcgccacacgcctcagggatttc 25

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 569238

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Database: EST.*

1: em_estbda:*
2: em_estbda:*
3: em_estbda:*
4: em_estbda:*
5: em_estbda:*
6: em_estbda:*
7: em_estbda:*
8: em_estbda:*
9: gb_est1:*
10: gb_est2:*
11: gb_est3:*
12: gb_est4:*
13: gb_est5:*
14: gb_est6:*
15: em_estfun:*
16: em_estfun:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rnd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	15.6	62.4	62	14	CF885516 trico82xk
2	15.4	61.6	100	9	AA470378 nei10c02.s
3	14.4	57.6	82	9	A1256079 ui94g12.x
4	14.4	57.6	92	14	CB165114 44 A1falf

C	5	14.2	56.8	62	9	A1669171	A1669171 wb81c10.x
C	6	14.2	56.8	72	12	B1057939	B1057939 BU057939
C	7	14.2	56.0	41	12	B1907426	B1907426 603063502
C	8	14.2	56.0	96	9	AA065383	AA065383 m15e0c.r
C	9	14.2	56.0	97	28	A2600786	A2600786 IM0418F15
C	10	13.8	55.2	64	29	CG399846	CG399846 01S0423-0
C	11	13.8	55.2	64	29	CL002253	CL002253 02S0069-0
C	12	13.8	55.2	73	14	U44135	U44135 ENU44135 Ag
C	13	13.8	55.2	75	14	F13772	F13772 HSP27429 H
C	14	13.8	55.2	84	12	BM126072	BM126072 f05b10.x
C	15	13.8	55.2	94	28	A2921627	A2921627 1006030G0
C	16	13.6	54.4	45	14	CB209994	CB209994 OML00274
C	17	13.6	54.4	45	14	CB211074	CB211074 OML01354
C	18	13.6	54.4	45	14	CB213865	CB213865 OML04145
C	19	13.6	54.4	61	28	BH913033	BH913033 3526.1.38
C	20	13.6	54.4	76	9	AA566995	AA566995 1049 Ldb1
C	21	13.6	54.4	78	29	CG712371	CG712371 1119026B0
C	22	13.6	54.4	81	28	B2380126	B2380126 SALK_1146
C	23	13.6	54.4	91	14	R82154	R82154 5B5 Chromos
C	24	13.6	54.4	91	29	D86884	D86884 Human exon
C	25	13.6	54.4	92	29	DMS47093	AJ547093 Drosophila
C	26	13.6	54.4	92	29	HSWC24E11	X88251 H.asapiens D
C	27	13.6	54.4	100	28	B2595658	B2595658 SALK_0894
C	28	13.6	54.4	100	29	CG781268	CG781268 1123044C0
C	29	13.4	53.6	49	9	AA513131	AA513131 nh78f09.s
C	30	13.4	53.6	50	9	AU106807	AU106807 AU106807
C	31	13.4	53.6	57	29	CG717331	CG717331 1119048A0
C	32	13.4	53.6	63	29	CG554070	CG554070 OST167335
C	33	13.4	53.6	66	29	CG712601	CG712601 1119027G0
C	34	13.4	53.6	68	29	CG519780	CG519780 OST83993
C	35	13.4	53.6	79	9	AA778587	AA778587 af86f10.s
C	36	13.4	53.6	79	29	CG487857	CG487857 OST23557
C	37	13.4	53.6	80	29	AG217446	AG217446 Drosophila
C	38	13.4	53.6	82	12	B1908831	B1908831 60306402
C	39	13.4	53.6	82	29	AG219169	AG219169 Drosophila
C	40	13.4	53.6	85	9	A1014256	A1014256 am50d10.s
C	41	13.4	53.6	96	13	B0816046	B0816046 N059E07 P
C	42	13.4	53.6	98	28	B2763567	B2763567 SALK_1193
C	43	13.2	52.8	77	9	AT006310	AT006310 AT006310
C	44	13.2	52.8	77	9	AA491818	AA491818 ng16b12.s
C	45	13.2	52.8	91	14	CK108605	CK108605 1044P93 P

ALIGNMENTS

RESULT 1
CF885516
LOCUS
DEFINITION
trico82xk23.b11 T.reesei mycelial culture, Version 6 October 2003
ACCESSION
CF885516
VERSION
CF885516.1 GI:38140198
KEYWORDS
SOURCE
ORGANISM
Hypocrea jecorina (anamorph: Trichoderma reesei)
REFERENCE
1 (bases 1 to 62)
Hypocrea jecorina; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypocrea.
AUTHORS
Diener,S.E., Dankmeyer,L., Dunn-Coleman,N., Houfek,T.D.,
Mitchell,T.K., van Solingen,P., Teunissen,P.J.M., Ward,M. and
Dean,R.A.
TITLE
Analysis of the protein processing and secretion pathways in a
Trichoderma reesei EST dataset
JOURNAL
Contact: Ralph A. Dean
COMMENT
Unpublished (2003)
Fungal Genomics Laboratory
North Carolina State University
Campus Box 7251, Raleigh, NC 27695, USA
Tel: 919-513-0020
Fax: 919-513-0024
Email: ralph.dean@ncsu.edu
Seq primer: UT-F1 primer.

FEATURES Source

ORIGIN

Query Match 62.4%; Score 15.6; DB 14; Length 62;
Best Local Similarity 81.8%; Pred. No. 1.1e+04;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 GCGCCAACTGCTGAGGATTTT 25
40 GGAGACACCTGCTGAGGATTTT 61

RESULT 2 AA470378 100 bp mRNA linear EST 13-AUG-1997
LOCUS AA470378/c
DEFINITION ne10c02.s1 NCI_CGAP_C03 Homo sapiens CDNA clone IMAGE:880802 3',
ACCESSION AA470378
VERSION AA470378.1 GI:2197687
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 100)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@db-remail.nih.gov
Tissue Procurement: Elias Campo, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bdrip/image/image.html
Insert Length: 527 Std Error: 0.00
Seq primer: -41ml3 fwd. RT from Amersham
High quality sequence stop: 86.

FEATURES Source

Location/Qualifiers
1..62
/organism="Hypocrea jecorina"
/mol_type="mRNA"
/strain="QM6a"
/db_xref="taxon:51453"
/clone="tric082K23"
/dev_stage="mycelia"
/clone_lib="T.reesei mycelial culture, Version 6 October
2003"
/note="Vector: PREP3; Site 1: Not I/Sal I; Mycelial
culture grown from 24 hrs to 6 days with varying Carbon
and Nitrogen sources and concentrations."

ORIGIN

Query Match 61.6%; Score 15.4; DB 9; Length 100;
Best Local Similarity 76.0%; Pred. No. 1.6e+04;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 CGGCGCCAACTGCTGAGGATTTT 25
71 CTGCGCCAACTGCTGAGGATTTT 47

RESULT 3 A1256079 82 bp mRNA linear EST 12-NOV-1998
LOCUS A1256079
DEFINITION u194g12.x1 Sugano mouse liver m1a Mus musculus CDNA clone
IMAGE:1890118 3' similar to SW:COX3_RAT P05505 CYTOCHROME C OXIDASE
POLYPEPTIDE III ; mRNA sequence.
ACCESSION A1256079
VERSION A1256079.1 GI:3863604
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 82)
Mairal,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterson,R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Maria W/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:974442
Trace considered overall poor quality
Possible reversed clone; similarity on wrong strand
Seq primer: custom primer used
High quality sequence stop: 1.

FEATURES Source

Location/Qualifiers
1..82
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL"
/db_xref="taxon:10090"
/clone="IMAGE:1890118"
/sex="female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="Sugano mouse liver m1a"
/note="Organ: liver; Vector: pMT185-FL3; Site 1: DraIII
(CACTGATG); Site 2: DraIII (CACTGATG); 1st strand CDNA
was primed with an oligo(dT) primer
[ATGTGGCTTTTCTTTTCTTTT]; double-stranded CDNA was
ligated to a DraIII adaptor [TGTGGCTTCTAGTGG]
and cloned into distinct DraIII sites of the pMT185-FL3
vector (5' site CACTGATG, 3' site CACTGATG). XhoI should
be used to isolate the CDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sunio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCGCTCTTAAGCTGG and 3' end
primer CGACCTGACGCTGAGCACA."

ORIGIN

Query Match 57.6%; Score 14.4; DB 9; Length 82;
Best Local Similarity 75.0%; Pred. No. 4.2e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGGCCCACTGCTAGGATTTT 25

Db 4 GGGCTCCAAACCCCAAGGATGTT 27

RESULT 4

CB165114/c 92 bp mRNA linear EST 30-JAN-2003
LOCUS 44 Alfalfa developing flower bud library Medicago sativa cDNA, mRNA
DEFINITION

ACCESSION CB165114

VERSION CB165114.1 GI:28151240

KEYWORDS EST

SOURCE Medicago sativa

ORGANISM Medicago sativa

REFERENCE 1 (bases 1 to 92)

AUTHORS Barone, P., Rosellini, D., and Veronesi, F.

TITLE Isolation of expressed sequence tags from developing flowers of

female sterile and female fertile alfalfa plants

Unpublished (2002)

COMMENT Contact: Rosellini, D.

Dipartimento di Biologia Vegetale e Biotecnologie Agroambientali

University of Perugia

Borgo XX giugno 74, 06121, Perugia, Italy

Tel: +390755856211

Fax: +390755856224

Email: rosellini@unipg.it

POLYA=No.

FEATURES

source

1..92

/organism="Medicago sativa"

/mol_type="mRNA"

/db_xref="taxon:3879"

/dev_stage="From ovule primordia to anthesis"

/lab_host="B.coli"

/clone_lib="Alfalfa developing flower bud library"

/note="Organ: Developing flower buds; Vector: Invitrogen

PCR4 TOPO Vector; This EST was obtained with the cDNA-AFLP

method (Bachem et al. Plant Journal 9:745-753, 1996). Total

RNA was extracted from three female fertile and three

female sterile alfalfa plants from an F1 population

obtained by crossing the plants B17 and P13 (Rosellini et

al. Theoretical and Applied Genetics, 97:1 289-1295,

1998). Equal amounts of RNA from each fertile or sterile

plant were bulked and used for the cDNA-AFLP protocol.

The restriction endonucleases EcoRI and MseI were used.

Bands that were polymorphic between the female sterile and

female fertile bulks were isolated from the polyacrylamide

gel, cloned in a plasmid vector (Invitrogen PCR4 TOPO) and

sequenced using the M13F primer. The published sequence

begins and ends with the EcoRI (GAATTC) and MseI (TTAA)

recognition sequences, respectively. The technical help of

Francesco Panara is gratefully acknowledged."

Query Match 57.6%; Score 14.4; DB 14; Length 92;

Best Local Similarity 75.0%; Pred. No. 4.4e+04;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 GGGGCCCACTGCTAGGATTTT 25

Db 48 GGTAGTCAACTCTTATAGATTTT 25

RESULT 5

AI669171/c

LOCUS AI669171

DEFINITION WP81c10.xi NCI_CGAP_P28 Homo sapiens cDNA clone IMAGE:2312082 3',

mRNA sequence.

ACCESSION AI669171

VERSION AI669171.1 GI:4833945

KEYWORDS EST

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 62)

AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

Journal National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

CONTACT: Robert Strauberg, Ph.D.

Email: cgap@fremail.nih.gov

Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

cDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

found through the I.M.A.G.E. Consortium/LNL at:

www-bio.lnl.gov/bdr/image/image.html

Seq primer: -40UP from Gibco.

FEATURES

source

1..62

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:2312082"

/sex="male"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="NCI CGAP P28"

/note="Organ: prostate; Vector: pTZ19-Pac (Pharmacia)

with a modified polylinker. Plasmid DNA from the

normalized library NCI CGAP_P22 was prepared, and 86

circles were made in vitro. Following HAP purification,

this DNA was used as tracer in a subtractive hybridization

reaction. The driver was PCR-amplified cDNAs from a pool

of 5,000 clones made from the same library (cloneds

985608-986759, 1101192-110195, and 1217928-1220615).

Subtraction by Bento Soares and M. Fatima Bonaldo."

QY 6 GCCAAGCTGCAAGGATTT 24

Db 56 GCCAAGCTGCAAGGATTT 38

ORIGIN

Query Match 56.8%; Score 14.2; DB 9; Length 62;

Best Local Similarity 84.2%; Pred. No. 4.8e+04;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GCCAAGCTGCAAGGATTT 24

Db 56 GCCAAGCTGCAAGGATTT 38

RESULT 6

LOCUS BU057939

DEFINITION BU057939 NIBB Mochii normalized Xenopus tailbud library Xenopus

laevis cDNA clone XL103003 5', mRNA sequence.

ACCESSION BU057939

VERSION BU057939.1 GI:17492296

KEYWORDS EST

SOURCE Xenopus laevis (African clawed frog)

ORGANISM Xenopus laevis

REFERENCE 1 (bases 1 to 72)

AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;

Xenopodinae; Xenopus.

Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and

Kohara, Y.

TITLE
Journal
COMMENT
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadashi Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp
The information of this clone is available through the following
URL:
http://xenopus.nibb.ac.jp.

FEATURES
Source
Location/Qualifiers
1..72
/organism="Xenopus laevis"
/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="X10303"
/issue_type="whole embryo"
/dev_stage="stage 25"
/clone_lib="NIBB Mochii normalized Xenopus tailbud
library"

ORIGIN

Query Match 56.8%; Score 14.2; DB 12; Length 72;
Best Local Similarity 72.7%; Pred. No. 5e+04;
Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
CY 4 GCGCCACCTGCTAGGATTTT 25
17 GTGCCAAGCTTNTGGGATTTT 38

RESULT 7
LOCUS BI907426 41 bp mRNA linear EST 16-OCT-2001
DEFINITION 603063502F1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5212728 5',
ACCESSION BI907426
VERSION BI907426.1 GI:16170258
KEYWORDS EST.
SOURCE Homo sapiens
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 41)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rcmail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11534 row: C column: 01
High quality sequence stop: 41.
Location/Qualifiers

FEATURES

Source
1..41
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5212728"
/issue_type="leukocyte"
/lab_host="DH10B"
/clone_lib="NIH_MGC_118"
/note="Vector: pCMV-Sport6; Site 1: NotI; Site 2: EcoRV
(destroyed); RNA source leukocytes from anonymous pool of
non-activated adult donors. Library is oligo-dT primed
and directionally cloned (EcoRV site is destroyed upon

cloning). Average insert size 1.7 kb, insert size range
1.2-3.3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 027. Note:
this is a NIH_MGC Library."

ORIGIN

Query Match 56.0%; Score 14; DB 12; Length 41;
Best Local Similarity 77.3%; Pred. No. 5.2e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CY 3 GCGCCACCTGCTAGGATTT 24
9 GCGCCACCTGCTAGGATCT 30

RESULT 8
LOCUS AA065383/c 96 bp mRNA linear EST 03-FEB-1997
DEFINITION m151e06.r1 Stragatene mouse testis (#37308) Mus musculus cDNA
ACCESSION AA065383
VERSION AA065383.1 GI:1562664
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 96)
Marras M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisler, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.
The WashU-HMI Mouse EST Project
Unpublished (1996)
Contact: Marras M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -26ml3 rev1 ET from Amersham
High quality sequence stop: 90.
Location/Qualifiers

TITLE
Journal
COMMENT

FEATURES

Source
1..96
/organism="Mus musculus"
/mol_type="mRNA"
/strain="CD-1"
/db_xref="taxon:10090"
/clone="IMAGE:515554"
/sex="males"
/issue_type="testis"
/dev_stage="10-12 week old"
/lab_host="SOLR (kanamycin resistant)"
/clone_lib="Stratagene mouse testis (#37308)"
/note="Organ: testis; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
-5' adaptor sequence: 5' GAATTCGACGAG 3' -3' adaptor
sequence: 5' CTCGAGTTTCTTTTCTTTT 3' "

ORIGIN

Query Match 56.0%; Score 14; DB 9; Length 96;
Best Local Similarity 77.3%; Pred. No. 6.7e+04;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
CY 3 GCGCCACCTGCTAGGATTT 24

JOURNAL
COMMENT

population
Unpublished (2003)
Contact: Donald R. McCarty
Plant Molecular and Cellular Biology Program
University of Florida
PO 110690 Gainesville, FL 32611-0690, USA
Tel: 352-392-1928 x322
Email: drmc@ufl.edu

FEATURES

source

Sequence flanking probable Mu insertion site in UniformMu line:
0280069-08, Primer set: C
Class: transposon insertion site.
Location/Qualifiers
1..64

/organism="Zea mays"
/mol_type="genomic DNA"
/strain="W22 (ACR, bz1-m9)"
/db_xref="taxon:4577"
/clone="0280069-08C1-G08"
/note="Vector: TOPO-PCR4; DNA flanking Mu transposon
insertions in Mu inactive lines were extracted from the
UniformMu maize population by the thermo asymmetric
interlaced PCR (TAIL) protocol using primers specific for
the Mu terminal inverted repeat and a set of 16 arbitrary
primers. Amplicons were size enriched using Sepharose 400
spin columns and cloned into the TOPO PCR4 vector."

ORIGIN

Query Match

Best Local Similarity 55.2%; Score 13.8; DB 29; Length 64;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGCGCAACCTGCTAGGATTTT 25
Db 63 CGGTGTCCAACTCCTAGGATTTT 39

RESULT 12

LOCUS

U44135

DEFINITION

EU44135 Aspergillus nidulans cleistothecium linear EST 03-Apr-1996
CDNA clone SR0101, mRNA sequence.

ACCESSION

U44135

VERSION

U44135.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

Contact: Keon-Sang Chae
Chonbuk National University
Chonju, 561-756, S. Korea
Tel: +82-652-70-3340
Fax: +82-652-70-3345
Email: chae@chonbuknms.chonbuk.ac.kr.
Location/Qualifiers
1..73

/organism="Aspergillus nidulans"
/mol_type="mRNA"
/strain="FGSC4"
/db_xref="taxon:162425"
/clone="SR0101"
/issue_type="cleistothecium"
/cell_type="hull cell"
/dev_stage="sexual"

ORIGIN

/clone_1lb="Aspergillus nidulans cleistothecium"
/note="3'-directed cDNA clones; single-pass sequencing"

Query Match

Best Local Similarity 55.2%; Score 13.8; DB 14; Length 73;
Matches 18; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GCGGCGCAACCTGCTAGGATTTT 25
Db 15 CGGTGTCCAACTCCTAGGATTTT 39

RESULT 13

LOCUS

F33772

DEFINITION

F33772

ACCESSION

F33772

VERSION

F33772.1

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

FEATURES

source

ORIGIN

Query Match

Best Local Similarity 55.2%; Score 13.8; DB 14; Length 75;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 3 GCGGCGCAACCTGCTAGG 19
Db 5 GCGGCGCAACCTGCTAGG 21

Contact: Valle G.
CIRI Biotechnology Centre
University of Padua
Via Trieste 75, 35121 Padua, Italy
ABI Chromatograms and other information are available on WWW at
http://grip.bio.unipd.it.
Location/Qualifiers
1..75

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="s300010H07"
/sex="female"
/issue_type="pectoral muscle (after mastectomy)"
/note="Vector: pCDNAII (Invitrogen); Site 1: BstXI;
Site 2: NotI. The library was constructed by G.
Lanfanchi. This library is not subtracted nor normalized.
The first strand cDNA was primed with a biotinylated
(5'-biotin-AACCTGCTGAGCGCGCTTTT) primer
de cDNA was sonicated and size-selected in the range
350-550 bp. The 3' specific fragments were selected by
streptavidin coated magnetic beads, ligated to
non-palindromic BstXI adapters, NotI digested and
directionally cloned into BstXI-NotI cut pCDNAII vector."

VERSION	A2921627.1	GI:13393448
KEYWORDS	GSS.	
SOURCE	Zea mays	
ORGANISM	Zea mays	
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.	
REFERENCE	1. (bases 1 to 94)	
AUTHORS	Walbot, V	
TITLE	Maize genomic sequences found using engineered RescuEmu transposon	
JOURNAL	Unpublished (2001)	
COMMENT	Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 723 8221 Email: walbot@stanford.edu Plate: 1006030 row: 45 Class: transposon-tagged. Location/Qualifiers 1..94 /organism="Zea mays" /mol_type="genomic DNA" /cultivar="mixed background W23/A186/B73" /db_xref="taxon:4577" /tissue_type="leaf" /dev_stage="adult" /lab_host="DH10B" /clone_11b="1006 - RescuEmu Grid G" /note="Organ: leaf; Vector: RescuEmu (engineered from	

```

pbluescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuemtu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuemtu, go to the web
site 'www.zmmb.iastate.edu' and follow the links for
'Rescuemtu'. Grid G was grown at Stanford in 2000. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

```

THIS PAGE BLANK FOR

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:28:53 ; Search time 39.2857 Seconds

(without alignments)
353.151 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 CGGGCGCAACCTGCTGATTC 25

Scoring table: IDENTITY_NUC

Gap10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 939230

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database:

1: /cgn2_6/prodata/2/ina/5A.COMB.seq.*
2: /cgn2_6/prodata/2/ina/5B.COMB.seq.*
3: /cgn2_6/prodata/2/ina/6A.COMB.seq.*
4: /cgn2_6/prodata/2/ina/6B.COMB.seq.*
5: /cgn2_6/prodata/2/ina/PCUTS.COMB.seq.*
6: /cgn2_6/prodata/2/ina/backfile1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	68.0	22	3	US-09-102-830-31 Sequence 31, App1
2	16.6	66.4	42	1	US-08-105-483-160 Sequence 160, App
3	16.6	66.4	42	1	US-08-709-209-160 Sequence 160, App
4	16.6	66.4	42	1	US-08-303-275-48 Sequence 48, App1
5	16.6	66.4	42	1	US-08-458-101-160 Sequence 160, App
6	15.4	61.6	33	2	US-08-455-968E-62 Sequence 62, App1
7	15.4	61.6	33	4	US-09-758-282B-151 Sequence 151, App
8	15.4	61.6	37	4	US-09-552-950-22 Sequence 22, App1
9	14.4	57.6	70	4	US-09-393-171-22 Sequence 22, App1
10	14.2	56.8	24	1	US-08-068-945A-13 Sequence 13, App1
11	14.2	56.8	24	1	US-08-442-806-13 Sequence 13, App1
12	14.2	56.8	35	1	US-08-748-068-14 Sequence 14, App1
13	14	56.0	65	4	US-09-625-188-27 Sequence 27, App1
14	13.8	55.2	38	1	US-08-137-175A-18 Sequence 18, App1
15	13.8	55.2	38	3	US-08-479-017-18 Sequence 18, App1
16	13.8	55.2	60	1	US-08-441-430-12 Sequence 12, App1
17	13.8	55.2	70	3	US-09-306-405-20 Sequence 20, App1
18	13.6	54.4	61	3	US-08-463-682-22 Sequence 22, App1
19	13.4	53.6	26	4	US-09-495-066-10 Sequence 10, App1
20	13.4	53.6	48	2	US-08-418-848A-23 Sequence 23, App1
21	13.4	53.6	49	1	US-08-706-135-3 Sequence 3, App1
22	13.4	53.6	49	5	PCT-US95-16904-3 Sequence 3, App1
23	13.2	52.8	62	3	US-08-443-950-1 Sequence 1, App1
24	13.2	52.8	67	4	US-09-650-324A-64 Sequence 64, App1
25	13	52.0	27	4	US-09-234-827B-10 Sequence 10, App1
26	13	52.0	31	1	US-08-019-870-33 Sequence 33, App1
27	13	52.0	50	4	US-09-475-947A-186 Sequence 186, App

28	13	52.0	96	3	US-08-484-322-31 Sequence 31, App1
29	12.8	51.2	27	4	US-09-439-616-8 Sequence 8, App1
30	12.8	51.2	38	4	US-09-233-086-12 Sequence 12, App1
31	12.8	51.2	47	4	US-09-422-978-739 Sequence 739, App
32	12.8	51.2	78	1	US-08-639-763-14 Sequence 14, App1
33	12.8	51.2	78	4	US-09-171-755B-14 Sequence 14, App1
34	12.8	51.2	84	2	US-08-476-176B-23 Sequence 23, App1
35	12.8	51.2	84	3	US-08-127-721A-23 Sequence 23, App1
36	12.8	51.2	84	3	US-08-465-246A-23 Sequence 23, App1
37	12.8	51.2	97	3	US-08-836-561-56 Sequence 56, App1
38	12.8	51.2	97	4	US-09-434-122-56 Sequence 56, App1
39	12.6	50.4	20	3	US-08-866-340-49 Sequence 49, App1
40	12.6	50.4	20	3	US-09-103-875-55 Sequence 55, App1
41	12.6	50.4	33	4	US-09-336-945B-64 Sequence 64, App1
42	12.6	50.4	34	4	US-08-387-805-14 Sequence 14, App1
43	12.6	50.4	36	3	US-09-113-750A-48 Sequence 48, App1
44	12.6	50.4	78	2	US-08-829-876-22 Sequence 22, App1
45	12.6	50.4	78	4	US-09-234-874A-22 Sequence 22, App1

ALIGNMENTS

RESULT 1
US-09-102-830-31
Sequence 31, Application US/09102830
Patent No. 6001558
GENERAL INFORMATION:
APPLICANT: BACKUS, JOHN W
APPLICANT: ATWOOD, SUSAN M
APPLICANT: CASEY, ANN E
APPLICANT: RASMUSSEN, ERIC B
APPLICANT: CUMMINS, THOMAS J
TITLE OF INVENTION: AMPLIFICATION AND DETECTION OF HIV-1
TITLE OF INVENTION: AND/OR HIV-2
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: JOHNSON & JOHNSON
STREET: ONE JOHNSON & JOHNSON PLAZA
CITY: NEW BRUNSWICK
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 08933
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/102,830
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: OGDEN, STASIA L
REGISTRATION NUMBER: 36,228
REFERENCE/DOCKET NUMBER: CDS-137/SLO
TELEPHONE: 908-524-2819
TELEFAX: 908-524-2808
INFORMATION FOR SEQ ID NO: 31:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-102-830-31
Query Match 68.0%; Score 17; DB 3; Length 22;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGGGCGCAACCTGCTGCTA 17

Db 6 CGGCGCCACCTGCTA 22

RESULT 2
US-08-105-483-160

Sequence 160, Application US/08105483
Patent No. 5494807

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/105,483

FILING DATE: 12-AUG-1993

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 160:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-105-483-160

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 1; Length 42;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24

Db 9 GGGCATCAGCAGCTTAGGATTT 31

RESULT 3
US-08-709-209-160

Sequence 160, Application US/08709209
Patent No. 5762938

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE

NUMBER OF SEQUENCES: 462

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/709,209

FILING DATE: 21-AUG-1996

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/105,483

FILING DATE: 12-AUG-1993

APPLICATION NUMBER: US 07/847,951

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2400

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 840-3333

TELEFAX: (212) 840-0712

INFORMATION FOR SEQ ID NO: 160:

SEQUENCE CHARACTERISTICS:

LENGTH: 42 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-709-209-160

Query Match

Best Local Similarity 66.4%; Score 16.6; DB 1; Length 42;

Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGCGCCACCTGCTAGGATTT 24

Db 9 GGGCATCAGCAGCTTAGGATTT 31

RESULT 4
US-08-303-275-48

Sequence 48, Application US/08303275
Patent No. 576598

GENERAL INFORMATION:

APPLICANT: Paoletti, Enzo

APPLICANT: Taregila, James

TITLE OF INVENTION: IMMUNODEFICIENCY VIRUS RECOMBINANT

NUMBER OF SEQUENCES: 205

CORRESPONDENCE ADDRESS:

ADDRESSEE: Curtis, Morris & Safford

STREET: 530 Fifth Avenue

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10036

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/303,275

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/897,382

FILING DATE: 11-JUN-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frommer, William S.

REGISTRATION NUMBER: 25,506

REFERENCE/DOCKET NUMBER: 454310-2420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-275-48

Query Match 66.4%; Score 16.6; DB 1; Length 42;
Best Local Similarity 82.6%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGGGCCACCTGCTAGGATTT 24
Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 5
US-08-458-101-160
Sequence 160, Application US/08458101
Patent No. 5766599
GENERAL INFORMATION:
APPLICANT: Paolietti, Enzo
APPLICANT: Perkins, Marion E.
APPLICANT: Taylor, Jill
APPLICANT: Tartaglia, James
APPLICANT: No. 5766599ton, Elizabeth K.
APPLICANT: Riviere, Michel
APPLICANT: de Taisne, Charles
APPLICANT: Limbach, Keith J.
APPLICANT: Johnson, Gerard P.
APPLICANT: Pincus, Steven E.
APPLICANT: Cox, William I.
APPLICANT: Audonnet, Jean-Christophe Francis
APPLICANT: Gettig, Russell Robert
TITLE OF INVENTION: GENETICALLY ENGINEERED VACCINE
TITLE OF INVENTION: STRAIN
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Curtis, Morris & Safford
ADDRESSEE: c/o William S. Frommer
STREET: 530 Fifth Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458.101
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Frommer, William S.
REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2740
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 160:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-458-101-160

Query Match 66.4%; Score 16.6; DB 1; Length 42;
Best Local Similarity 82.6%; Pred. No. 22;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 GGGGGCCACCTGCTAGGATTT 24
Db 9 GGGCATCAGCAGCTAGGATTT 31

RESULT 6
US-08-455-968B-62/c
Sequence 62, Application US/08455968B
Patent No. 5874283
GENERAL INFORMATION:
APPLICANT: Harrington, John L.
APPLICANT: Hsieh, Chih-Lin
APPLICANT: Lieber, Michael
TITLE OF INVENTION: Mammalian Flap-Specific Endonuclease
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/455.968B
FILING DATE: 30-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 18985-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (oligonucleotide)
US-08-455-968B-62
Query Match 61.6%; Score 15.4; DB 2; Length 33;
Best Local Similarity 76.0%; Pred. No. 86;
Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 GGGGGCCACCTGCTAGGATTT 25
Db 31 CGACCTGACAGCTGCTAGGATTT 7

RESULT 7
US-09-758-282B-151
Sequence 151, Application US/09758282B
Patent No. 6635463
GENERAL INFORMATION:
APPLICANT: Ma, Wu-Po
APPLICANT: Yamichev, Victor I.
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamicheva, Natalie E.
APPLICANT: Allawi, Hatim T.
APPLICANT: Schaefer, James J.
APPLICANT: Neri, Bruce P.

/ TITLE OF INVENTION: Enzymes for the Detection of Nucleic Acid Sequences

/ FILE REFERENCE: FORS 04931

/ CURRENT APPLICATION NUMBER: US/09/758,282B

/ PRIOR FILING DATE: 2001-01-11

/ PRIOR APPLICATION NUMBER: 09/577,304

/ PRIOR FILING DATE: 2000-05-24

/ NUMBER OF SEQ ID NOS: 280

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 151

/ LENGTH: 33

/ TYPE: DNA

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-09-758-282B-151

Query Match

Best Local Similarity 61.6%; Score 15.4; DB 4; Length 33;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db

5 CGGCACTGCTAGGGA 21

3 CGGCACTGCTAGGGA 19

RESULT 8

US-09-552-950-22

/ Sequence 22, Application US/09552950

/ Patent No. 6541248

/ GENERAL INFORMATION:

/ APPLICANT: Oxford Biomedica (UK) Limited

/ TITLE OF INVENTION: Anti-Viral Vectors

/ FILE REFERENCE: 674524-2004

/ CURRENT APPLICATION NUMBER: US/09/552,950

/ CURRENT FILING DATE: 2000-04-20

/ NUMBER OF SEQ ID NOS: 22

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 22

/ LENGTH: 37

/ TYPE: DNA

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence:primer RIB3

US-09-552-950-22

Query Match

Best Local Similarity 61.6%; Score 15.4; DB 4; Length 37;

Matches 19; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db

1 CGGGCGCCACCTGCTAGGATTTT 25

12 CGGGCGCCACCTGCTAGGATTTT 36

RESULT 9

US-09-393-171-22

/ Sequence 22, Application US/09393171

/ Patent No. 6673569

/ GENERAL INFORMATION:

/ APPLICANT: KUROKAWA, Yoichi

/ APPLICANT: YANAGI, Hideki

/ APPLICANT: YURA, Takeshi

/ TITLE OF INVENTION: Dsba/Dsbb/Dsbc/Dsbd expression plasmid

/ FILE REFERENCE: 1422-391P

/ CURRENT APPLICATION NUMBER: US/09/393,171

/ CURRENT FILING DATE: 1999-09-09

/ EARLIER APPLICATION NUMBER: JP 10/255702

/ EARLIER FILING DATE: 1998-09-09

/ NUMBER OF SEQ ID NOS: 25

/ SEQ ID NO 22

/ LENGTH: 70

/ TYPE: DNA

/ ORGANISM: Artificial Sequence

US-09-393-171-22

Query Match

Best Local Similarity 57.6%; Score 14.4; DB 4; Length 70;

Matches 18; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Db

2 GGGCGCACTGCTAGGATTTT 25

3 GGGCGCACTGCTAGGATTTT 26

RESULT 10

US-08-068-945A-13/C

/ Sequence 13, Application US/08068945A

/ Patent No. 5616483

/ GENERAL INFORMATION:

/ APPLICANT: Bjursell, Gunnar

/ APPLICANT: Carlsson, Peter

/ APPLICANT: Enerback, Sven

/ APPLICANT: Hansson, Lennart

/ APPLICANT: Lidberg, Ulf

/ APPLICANT: Nilsson, Jeanette

/ APPLICANT: Tornell, Jan

/ TITLE OF INVENTION: New DNA Sequences

/ NUMBER OF SEQUENCES: 58

/ CORRESPONDENCE ADDRESSES:

/ ADDRESSER: White & Case

/ STREET: 1155 Avenue of the Americas

/ CITY: New York

/ STATE: New York

/ COUNTRY: United States

/ ZIP: 10036-2787

/ COMPUTER READABLE FORM:

/ MEDIUM TYPE: Floppy disk

/ COMPUTER: IBM PC compatible

/ OPERATING SYSTEM: PC-DOS/MS-DOS

/ SOFTWARE: PatentIn Release #1.0, Version #1.25

/ CURRENT APPLICATION DATA:

/ APPLICATION NUMBER: US/08/068,945A

/ FILING DATE: 27-MAY-1993

/ CLASSIFICATION: 435

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: SE 9201809-2

/ FILING DATE: 11-JUN-1992

/ PRIOR APPLICATION DATA: SE 9201826-6

/ FILING DATE: 12-JUN-1992

/ PRIOR APPLICATION DATA: SE 9202088-2

/ FILING DATE: 03-JUL-1992

/ PRIOR APPLICATION DATA:

/ APPLICATION NUMBER: SE 9300902-5

/ FILING DATE: 19-MAR-1993

/ ATTORNEY/AGENT INFORMATION:

/ NAME: Steiner, Richard J.

/ REGISTRATION NUMBER: 35,372

/ TELECOMMUNICATION INFORMATION:

/ TELEPHONE: (212)819-8783

/ TELEFAX: (212)354-8113

/ INFORMATION FOR SEQ ID NO: 13:

/ SEQUENCE CHARACTERISTICS:

/ LENGTH: 24 base pairs

/ TYPE: nucleic acid

/ STRANDEDNESS: single

/ TOPOLOGY: linear

/ MOLECULE TYPE: DNA (genomic)

US-08-068-945A-13

Query Match

Best Local Similarity 56.8%; Score 14.2; DB 1; Length 24;

Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGCCCAACTGCTAGGGA 21
|||||
Db 24 GCGGCCCAACTGCTAGGGA 6

RESULT 11
US-08-442-806-13/c
; Sequence 13, Application US/08442806
; Patent No. 5716817
; GENERAL INFORMATION:
; APPLICANT: Bjursell, Gunnar
; APPLICANT: Carlsson, Peter
; APPLICANT: Enerback, Sven
; APPLICANT: Hansson, Lennart
; APPLICANT: Lidberg, Ulf
; APPLICANT: Nilsson, Jeanette
; APPLICANT: Tornell, Jan
; TITLE OF INVENTION: Genomic DNA Sequences
; TITLE OF INVENTION: Encoding Human BSL/CEL
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Cage
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,806
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/068,945
; FILING DATE: 27-MAY-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201809-2
; FILING DATE: 11-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9201826-6
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9202088-2
; FILING DATE: 03-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9300902-5
; FILING DATE: 19-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Sterner, Richard J.
; REGISTRATION NUMBER: 35,372
; REFERENCE/DOCKET NUMBER: 1103326-052
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)819-8783
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-442-806-13

Query Match 56.8%; Score 14.2; DB 1; Length 24;
Best Local Similarity 84.2%; Pred. No. 3.3e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 GCGGCCCAACTGCTAGGGA 21

Db 24 GCGGCCCAACTGCTAGGGA 6
|||||

RESULT 12
US-08-748-068-14
; Sequence 14, Application US/08748068
; Patent No. 5770410
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Chiral Synthesis
; NUMBER OF SEQUENCES: 15
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/748,068
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/256,959
; FILING DATE: 05-OCT-1994
; APPLICATION NUMBER: GB 92 02033.8
; FILING DATE: 30-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 92 04702.6
; FILING DATE: 04-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 93/00204
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-748-068-14

Query Match 56.8%; Score 14.2; DB 1; Length 35;
Best Local Similarity 84.2%; Pred. No. 3.5e+02;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GCGGCCCAACTGCTAGG 19
|||||
Db 6 GCGGCCCAACTGCTAGG 24

RESULT 13
US-09-625-188-27
; Sequence 27, Application US/09625188
; Patent No. 6307037
; GENERAL INFORMATION:
; APPLICANT: No. 6307037artis AG
; TITLE OF INVENTION: Fungal Target Genes and Methods
; FILE REFERENCE: PB/5-31285p1
; CURRENT APPLICATION NUMBER: US/09/625,188
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 27
; LENGTH: 65
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: oligonucleotide
; US-09-625-188-27

Query Match 56.0%; Score 14; DB 4; Length 65;
Best Local Similarity 77.3%; Pred. No. 5e+02;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:37:23 ; Search time 1822.08 Seconds
(without alignments)
67.525 Million cell updates/sec

Title: US-10-001-407-10

Perfect score: 25

Sequence: 1 CGGGCGCAACCTGCTAGGATCTT 25

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3237270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 2018620

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/prodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/prodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/prodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/prodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/prodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/prodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/prodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/prodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/prodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/prodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/prodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/prodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	100.0	25	14	US-10-001-407-10
2	25	100.0	34	14	US-10-001-407-8
3	25	100.0	34	14	US-10-001-407-9
4	25	100.0	52	14	US-10-001-407-15
5	18	72.0	25	14	US-10-001-407-14
6	18	72.0	58	14	US-10-001-407-13
7	16.6	66.4	24	14	US-10-001-407-13
8	16.6	66.4	57	14	US-10-001-407-18
9	16.2	64.8	100	15	US-10-272-665-108
10	16.2	64.8	100	15	US-10-272-665-109
11	16.2	64.8	100	15	US-10-273-321-108
12	16.2	64.8	100	15	US-10-273-321-109
13	16.2	64.8	100	15	US-10-272-756-108
14	16.2	64.8	100	15	US-10-272-756-109

15	16.2	64.8	100	16	US-10-273-228-108	Sequence 108, App
16	16.2	64.8	100	16	US-10-273-228-109	Sequence 109, App
17	15.4	61.6	33	10	US-09-864-636A-292	Sequence 292, App
18	15.4	61.6	33	10	US-09-758-282-151	Sequence 151, App
19	15.4	61.6	33	11	US-09-864-426A-292	Sequence 292, App
20	15.4	61.6	33	15	US-10-084-839-292	Sequence 292, App
21	15.4	61.6	37	9	US-09-999-183-21	Sequence 21, App
22	15.4	61.6	37	16	US-10-351-838-22	Sequence 22, App
23	15.2	60.8	95	15	US-10-126-474A-12	Sequence 12, App
24	14.8	59.2	20	15	US-10-126-474A-1	Sequence 1, App
25	14.4	57.6	65	15	US-10-251-364-23	Sequence 23, App
26	14.4	57.6	65	16	US-10-351-196-24	Sequence 24, App
27	14.4	57.6	65	16	US-10-463-980-26	Sequence 26, App
28	14.4	57.6	86	16	US-10-379-992A-10	Sequence 10, App
29	14.4	57.6	90	14	US-10-003-035-74	Sequence 74, App
30	14.4	57.6	90	15	US-10-286-332A-74	Sequence 74, App
31	14.4	57.6	90	16	US-10-280-915-74	Sequence 74, App
32	14.2	56.8	67	10	US-09-931-325A-99	Sequence 99, App
33	14.2	56.8	67	10	US-09-930-915A-140	Sequence 140, App
34	14.2	56.8	67	15	US-10-082-014-255	Sequence 255, App
35	14.2	56.8	67	15	US-10-372-076-285	Sequence 285, App
36	14.2	56.8	67	17	US-10-806-006-140	Sequence 140, App
37	14.2	56.8	67	17	US-10-677-074-285	Sequence 285, App
38	14.2	56.8	67	17	US-10-805-913-140	Sequence 140, App
39	14.2	56.8	75	10	US-09-931-325A-98	Sequence 98, App
40	14.2	56.8	75	15	US-10-082-014-254	Sequence 254, App
41	14.2	56.8	75	15	US-10-372-076-284	Sequence 284, App
42	14.2	56.8	75	17	US-10-806-006-139	Sequence 139, App
43	14.2	56.8	75	17	US-10-677-074-284	Sequence 284, App
44	14.2	56.8	75	17	US-10-805-913-139	Sequence 139, App
45	14.2	56.8	75	17	US-10-805-913-139	Sequence 139, App

ALIGNMENTS

RESULT 1
US-10-001-407-10
; Sequence 10, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001.407
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 25
; TYPE: DNA
; ORGANISM: HIV-2
; US-10-001-407-10

Query Match 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGGGCGCAACCTGCTAGGATTTT 25
DB 1 CGGGCGCAACCTGCTAGGATTTT 25

RESULT 2
US-10-001-407-8/c
; Sequence 8, Application US/10001407
; Publication No. US20020177127A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 8
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-8
```

```
Query Match
Best Local Similarity 100.0%; Score 25; DB 14; Length 34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGCGCCCAACCTGCTAGGATTTT 25
Db 25 CGGCGCCCAACCTGCTAGGATTTT 1
```

```
RESULT 3
US-10-001-407-9
/ Sequence 9, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 9
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-9
```

```
Query Match
Best Local Similarity 100.0%; Score 25; DB 14; Length 34;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGCGCCCAACCTGCTAGGATTTT 25
Db 10 CGGCGCCCAACCTGCTAGGATTTT 34
```

```
RESULT 4
US-10-001-407-15
/ Sequence 15, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 15
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-15
```

```
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 15
/ LENGTH: 52
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: T7 promoter primer having a promoter sequence
/ OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
US-10-001-407-15
```

```
Query Match
Best Local Similarity 100.0%; Score 25; DB 14; Length 52;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGCGCCCAACCTGCTAGGATTTT 25
Db 28 CGGCGCCCAACCTGCTAGGATTTT 52
```

```
RESULT 5
US-10-001-407-14
/ Sequence 14, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 14
/ LENGTH: 25
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-14
```

```
Query Match
Best Local Similarity 100.0%; Score 18; DB 14; Length 25;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGGCGCCCAACCTGCTAG 18
Db 8 CGGCGCCCAACCTGCTAG 25
```

```
RESULT 6
US-10-001-407-19
/ Sequence 19, Application US/10001407
/ Publication No. US20020177127A1
/ GENERAL INFORMATION:
/ APPLICANT: Yang, Yeasing
/ APPLICANT: Burrell, Terrie
/ TITLE OF INVENTION: Compositions and Methods for Detecting
/ FILE REFERENCE: GP117-03.UT
/ CURRENT FILING DATE: 2001-10-22
/ PRIOR APPLICATION NUMBER: 60/242,620
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/280,058
/ PRIOR FILING DATE: 2001-03-30
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO: 19
/ LENGTH: 34
/ TYPE: DNA
/ ORGANISM: HIV-2
US-10-001-407-19
```

```
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 19
; LENGTH: 58
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
; OTHER INFORMATION: primer sequence
US-10-001-407-19
```

```
Query Match      72.0%; Score 18; DB 14; Length 58;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 CGGGCGCCACCTGCTAG 18
Db      41 CGGGCGCCACCTGCTAG 58
```

RESULT 7

```
US-10-001-407-13
; Sequence 13, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer mismatches HIV-2 sequence by deletion of
; OTHER INFORMATION: one nucleotide
US-10-001-407-13
```

```
Query Match      66.4%; Score 16.6; DB 14; Length 24;
Best Local Similarity 82.6%; Pred. No. 1.8e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      3 GGGCGCCACCTGCTAGGATTT 25
Db      2 GGGCGCCACCTGCTAGGATTT 24
```

RESULT 8

```
US-10-001-407-18
; Sequence 18, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Burrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
```

```
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
; OTHER INFORMATION: SEQ ID NO:13
US-10-001-407-18
```

```
Query Match      66.4%; Score 16.6; DB 14; Length 57;
Best Local Similarity 82.6%; Pred. No. 1.9e+02;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

```
OY      3 GGGCGCCACCTGCTAGGATTT 25
Db      35 GGGCGCCACCTGCTAGGATTT 57
```

RESULT 9

```
US-10-272-665-108
; Sequence 108, Application US/10272665
; Publication No. US20030180748A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI
; TITLE OF INVENTION: GENETIC MARKERS
; FILE REFERENCE: 24736-2033E
; CURRENT APPLICATION NUMBER: US/10/272,665
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Hom sapien
US-10-272-665-108
```

```
Query Match      64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 GGGCGCCACCTGCTAGGAT 22
Db      64 GGGCGTCACCTGCAAGTAT 84
```

RESULT 10

```
US-10-272-665-109
; Sequence 109, Application US/10272665
; Publication No. US20030180748A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING POI
; TITLE OF INVENTION: GENETIC MARKERS
; FILE REFERENCE: 24736-2033E
; CURRENT APPLICATION NUMBER: US/10/272,665
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
```

```

; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-665-109
```

```
Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```
RESULT 11
US-10-273-321-108
; Sequence 108, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033B
; CURRENT APPLICATION NUMBER: US/10/273,321
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-108
```

```
Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```
RESULT 12
US-10-273-321-109
; Sequence 109, Application US/10273321
; Publication No. US20030180749A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033B
```

```

; CURRENT APPLICATION NUMBER: US/10/273,321
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-321-109
```

```
Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```
RESULT 13
US-10-272-756-108
; Sequence 108, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033C
; CURRENT APPLICATION NUMBER: US/10/272,756
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-108
```

```
Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGTAT 84
```

```
RESULT 14
US-10-272-756-109
; Sequence 109, Application US/10272756
; Publication No. US20030190644A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
```

```
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033C
; CURRENT APPLICATION NUMBER: US/10/272,756
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-272-756-109
```

```
Query Match          64.8%; Score 16.2; DB 15; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGSTAT 84
```

```
RESULT 15
US-10-273-228-108
; Sequence 108, Application US/10273228
; Publication No. US20030207297A1
; GENERAL INFORMATION:
; APPLICANT: Braun et al.
; TITLE OF INVENTION: METHODS FOR GENERATING DATABASES AND DATABASES FOR IDENTIFYING PC
; FILE REFERENCE: 24736-2033D
; CURRENT APPLICATION NUMBER: US/10/273,228
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/687,483
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/217,658
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 60/159,176
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: 60/217,251
; PRIOR FILING DATE: 2000-07-10
; PRIOR APPLICATION NUMBER: 09/663,968
; PRIOR FILING DATE: 2000-09-19
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 108
; LENGTH: 100
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-273-228-108
```

```
Query Match          64.8%; Score 16.2; DB 16; Length 100;
Best Local Similarity 85.7%; Pred. No. 3.1e+02;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

```
OY      2 GGGCGCCAACTGCTAGGAT 22
        |||||
Db      64 GGGCGTCAACTGCAAGSTAT 84
```

Search completed: August 31, 2004, 06:17:02
Job time : 1823.08 secs

THIS PAGE BLANK (use)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:20:52 ; Search time 1095.38 Seconds

(without alignments)
2057.592 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52
Sequence: 1 aacttaatacgaactcactat.....gccaaactgctaggatttc 52

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 1846492

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:*

1: gb_ba:*

2: gb_hcg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_stc:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_da:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_ph:*

24: em_pat:*

25: em_pl:*

26: em_ro:*

27: em_stc:*

28: em_un:*

29: em_vi:*

30: em_hcg_hum:*

31: em_hcg_inv:*

32: em_hcg_other:*

33: em_hcg_mus:*

34: em_hcg_pln:*

35: em_hcg_rtd:*

36: em_hcg_mam:*

37: em_hcg_vrc:*

38: em_sy:*

39: em_hcgo_hum:*

40: em_hcgo_mus:*

41: em_hcgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	52	6	AX498427 Sequence
2	36.4	70.0	50	6	AR400936 Sequence
3	36.4	70.0	50	6	AX074095 Sequence
4	36.4	70.0	50	6	AX498429 Sequence
5	36.4	70.0	51	6	AR400954 Sequence
6	36.4	70.0	51	6	AX074113 Sequence
7	36	69.2	54	6	E61328 Probe for d
8	36	69.2	54	6	AR352014 Sequence
9	31.8	61.2	52	6	AR344818 Sequence
10	31.8	61.2	52	6	AX397773 Sequence
11	31.4	60.4	49	6	BD236963 Nucleic a
12	31.4	60.4	49	6	AR307449 Sequence
13	31.4	60.4	52	6	AX025599 Sequence
14	31.2	60.0	47	6	A99135 Sequence 9
15	31.2	60.0	47	6	BD080307 Nucleic a
16	30.4	58.5	52	6	E61341 Probe for d
17	30.4	58.5	52	6	AR352027 Sequence
18	30.2	58.1	50	6	AX397771 Sequence
19	30.2	58.1	50	6	AR344816 Sequence
20	30.2	58.1	53	6	AR344848 Sequence
21	30.2	58.1	48	6	AX397803 Sequence
22	29.8	57.3	48	6	AR210629 Sequence
23	29.8	57.3	48	6	AR232027 Sequence
24	29.8	57.3	48	6	AR399645 Sequence
25	29.8	57.3	48	6	AX391328 Sequence
26	29.6	56.9	47	6	AR070666 Sequence
27	29.6	56.9	47	6	AR157485 Sequence
28	29.6	56.9	47	6	BD243351 Protectio
29	29.6	56.9	47	6	125930 Sequence 10
30	29.6	56.9	47	6	BD132855 Methode o
31	29.4	56.5	51	6	AX708731 Sequence
32	29.2	56.2	45	6	E61325 Probe for d
33	29.2	56.2	45	6	AR352051 Sequence
34	29.2	56.2	47	6	AX721018 Sequence
35	29.2	56.2	53	6	AX802772 Sequence
36	29.2	56.2	53	6	AX803190 Sequence
37	28.8	55.4	48	6	AR400952 Sequence
38	28.8	55.4	48	6	AX074111 Sequence
39	28.8	55.4	49	6	AR400956 Sequence
40	28.8	55.4	49	6	AX074115 Sequence
41	28.8	55.4	50	6	AR344819 Sequence
42	28.8	55.4	50	6	AX397774 Sequence
43	28.8	55.4	53	6	140641 Sequence 13
44	28.8	55.4	53	6	140642 Sequence 14
45	28.8	55.4	53	6	140643 Sequence 15

ALIGNMENTS

RESULT 1
AX498427
LOCUS AX498427 52 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 15 from Patent WO0234951.
ACCESSION AX498427
VERSION AX498427.1 GI:23343305
KEYWORDS
SOURCE
ORGANISM
synthetic construct
artificial sequences.
REFERENCE
1 Yang, Y.Y. and Burrell, T.A.
AUTHORS Compositions and methods for detecting human immunodeficiency virus
TITLE 2 (hiv-2)
JOURNAL Patent: WO 0234951-A 15 02-MAY-2002;

FEATURES
source
Gen-Probe Incorporated (US)
Location/Qualifiers
1..52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of an HIV-2 complementary primer
sequence"

ORIGIN
Query Match 100.0%; Score 52; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 8.6e-10;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52

RESULT 2
AR400936
LOCUS AR400936 50 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 8 from patent US 6623920.
ACCESSION AR400936
VERSION AR400936.1 GI:40148228
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 50)
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.H.
TITLE Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: US 6623920-A 8 23-SEP-2003;
FEATURES Location/Qualifiers
1..50
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 50;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 50

RESULT 3
AX074095
LOCUS AX074095 50 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 8 from Patent WO0104361.
ACCESSION AX074095
VERSION AX074095.1 GI:12710307
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D.P., Giachetti,C. and McDonough,S.H.
TITLE Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: WO 0104361-A 8 18-JAN-2001;
Gen-Probe Incorporated (US) ; Bee, Gary G. (US) ; Yang, Yeasing Y.
(US) ; Kolk, Dan P. (US) ; Giachetti, Cristina (US) ; McDonough,
Sherrol Hoffa (US)
FEATURES Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic amplification oligomer with 5' promoter
sequence, for HIV-1 LTR region"

ORIGIN

Query Match 70.0%; Score 36.4; DB 6; Length 50;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 50

RESULT 4
AX498429
LOCUS AX498429 50 bp DNA linear PAT 26-SEP-2002
DEFINITION Sequence 17 from Patent WO0234951.
ACCESSION AX498429
VERSION AX498429.1 GI:23343307
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Yang,Y.Y. and Burrell,T.A.
TITLE Compositions and methods for detecting human immunodeficiency virus
JOURNAL Patent: WO 0234951-A 17 02-MAY-2002;
Gen-Probe Incorporated (US)
FEATURES Location/Qualifiers
1..50
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="T7 promoter primer having a promoter sequence
appended at the 5' end of the sequence given as SEQ ID
NO:12"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 50;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 50

RESULT 5
AR400954
LOCUS AR400954 51 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 26 from patent US 6623920.
ACCESSION AR400954
VERSION AR400954.1 GI:40148246
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 51)
AUTHORS Bee,G.G., Yang,Y.Y., Kolk,D., Giachetti,C. and McDonough,S.H.
TITLE Detection of HIV-1 by nucleic acid amplification
JOURNAL Patent: US 6623920-A 26 23-SEP-2003;
FEATURES Location/Qualifiers
1..51
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 51;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGGCGGCAACTGCTAGGATTTT 50

RESULT 6
AX074113
LOCUS AX074113 51 bp DNA linear PAT 06-FEB-2001
DEFINITION Sequence 26 from Patent WO0104361.
ACCESSION AX074113
VERSION AX074113.1 GI:12710325
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
1 Bee,G., Yang,Y.Y., Kolk,D.P., Giachetti,C. and McDonough,S.H.
Detection of hiv-1 by nucleic acid amplification
Patent: WO 0104361-A 26 18-JUN-2001;
Gen-Probe Incorporated (US) ; Bee, Gary G. (US) ; Yang, Yeasing Y.
(US) ; Kolk, Dan P. (US) ; Giachetti, Cristelina (US) ; McDonough,
Sherrol Hoffa (US)
JOURNAL
FEATURES
source Location/Qualifiers
1..51
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="synthetic amplification oligomer with 5' promoter
sequence, for HIV-1 LTR region"

ORIGIN
Query Match 70.0%; Score 36.4; DB 6; Length 51;
Best Local Similarity 94.2%; Pred. No. 0.0016;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
OY 1 AATTATACGACTACTATAGGAGACGGCGCCACCTGCTAGGATTT 52
1 AATTATACGACTACTATAGGAGACGGCGCCCA--CTGCTAGGATTT 50
Db 1 AATTATACGACTACTATAGGAGACGGCGCCCA--CTGCTAGGATTT 50

RESULT 7
E61328
LOCUS E61328 54 bp DNA linear PAT 18-JUN-2001
DEFINITION Probe for detecting oligonucleotide.
ACCESSION E61328
VERSION E61328.1 GI:13025890
KEYWORDS JP 199046778-A/2.
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
1 (bases 1 to 54)
AUTHORS Daniel,L.K. and Timothy,J.F.
TITLE Probe for detecting oligonucleotide
JOURNAL Patent: JP 199046778-A 2 23-FEB-1999;
GEN-PROB INC
COMMENT OS Artificial Sequence
PN JP 199046778-A/2
PD 23-FEB-1999
PR 14-JAN-1998 JP 1998005607
PI 11-JUL-1989 US 379501
PT DANIEL LOUIS KASHIAN,TIMOTHY J FURUTSU
PC C12N15/09,C12Q1/68,C12N15/00
CC
FH Key Location/Qualifiers
FT source 1..54
/organism="Artificial Sequence".
Location/Qualifiers
1..54
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 69.2%; Score 36; DB 6; Length 54;
Best Local Similarity 80.8%; Pred. No. 0.0023;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

OY 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52
1 AATTATACGACTACTATAGGAGACGAGGACTTCCGCTGGGACTTT 52
Db 1 AATTATACGACTACTATAGGAGACGAGGACTTCCGCTGGGACTTT 52

RESULT 8
AR352014
LOCUS AR352014 54 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6589734.
ACCESSION AR352014
VERSION AR352014.1 GI:33756977
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
1 (bases 1 to 54)
AUTHORS Kacian,D.L., Fultz,T.J. and McDonough,S.H.
TITLE Detection of HIV
JOURNAL Patent: US 6589734-A 2 08-JUL-2003;
FEATURES
source Location/Qualifiers
1..54
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 69.2%; Score 36; DB 6; Length 54;
Best Local Similarity 80.8%; Pred. No. 0.0023;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 52
1 AATTATACGACTACTATAGGAGACGAGCAAGGACTTCCGCTGGGACTTT 52
Db 1 AATTATACGACTACTATAGGAGACGAGCAAGGACTTCCGCTGGGACTTT 52

RESULT 9
AR344818
LOCUS AR344818 52 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 7 from patent US 6582920.
ACCESSION AR344818
VERSION AR344818.1 GI:33740899
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1
1 (bases 1 to 52)
AUTHORS Yang,Y.Y., Brentano,S.T., Babola,O., Tran,N. and Vernet,G.
TITLE Amplification of HIV-1 RT sequences for detection of sequences
associated with drug-resistance mutations
JOURNAL Patent: US 6582920-A 7 24-JUN-2003;
FEATURES
source Location/Qualifiers
1..52
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 61.2%; Score 31.8; DB 6; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.11;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1 AATTATACGACTACTATAGGAGACGGCGCCCACTGCTAGGATTT 51
1 AATTATACGACTACTATAGGAGACGAGCAAGGACTTCCGCTGGGACTTT 51
Db 1 AATTATACGACTACTATAGGAGACGAGCAAGGACTTCCGCTGGGACTTT 51

RESULT 10
AX397773
LOCUS AX397773 52 bp DNA linear PAT 27-MAY-2002
DEFINITION Sequence 7 from Patent WO0220852.
ACCESSION AX397773
VERSION AX397773.1 GI:21260647
KEYWORDS
SOURCE synthetic construct

ORGANISM synthetic construct
artificial sequences.

REFERENCE
1 Yang, Y.Y., Brenbano, S.T., Babola, O., Tran, N. and Vernet, G.
Amplification of hiv-1 sequences for detection of sequences
associated with drug-resistance mutations
Patent: WO 0220852-A 7 14-MAR-2002;
Gen-Probe Incorporated Patent Dept (US) ; Biomerieux S.A. (FR)

FEATURES
source
1. .52
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotide primer for Protease target
sequence"
1. .32

ORIGIN
Promoter
1. .32

Query Match 61.2%; Score 31.8; DB 6; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.11; 12; Indels 0; Gaps 0;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTGCTAGGATT 51
1 AATTATACGACTCACTATAGGAGACCGACCATCATCTGCTGCTT 51

Db 1 AATTATACGACTCACTATAGGAGACCGACCATCATCTGCTGCTT 51

RESULT 11
BD236963 49 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Nucleic acid sequence for detecting genetic marker for cancer in
biological samples.
ACCESSION BD236963
VERSION BD236963.1 GI:33046733
KEYWORDS JP 2002535014-A/38.
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE
1 (bases 1 to 49)
Harvey, R.C. and Jr, T.J.C.
Nucleic acid sequence for detecting genetic marker for cancer in
biological samples
Patent: JP 2002535014-A 38 22-OCT-2002;
JOURNAL
GEN PROBE INC
COMMENT
OS Artificial Sequence
PN JP 2002535014-A/38
PF 22-OCT-2002
PR 28-JAN-2000 JP 2000596180
PI RICHARD C HARVEY, THOMAS J CLARK JR
PC C12N15/09, C1201/68, C12N15/00
CC Description of Artificial Sequence: synthetic construct FH
Key Location/Qualifiers
FT promoter
Location/Qualifiers
1. .49
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 60.4%; Score 31.4; DB 6; Length 49;
Best Local Similarity 85.4%; Pred. No. 0.16; 6; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTG 41
2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

Db 2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

RESULT 12
AR307449 49 bp DNA linear PAT 12-JUN-2003
LOCUS
AR307449 49 bp DNA linear PAT 12-JUN-2003

DEFINITION Sequence 38 from patent US 6551778.
ACCESSION AR307449
VERSION AR307449.1 GI:31697988
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 49)
Harvey, R.C. and Clark, T.J. Jr.
Nucleic acid sequences for detecting genetic markers for cancer in
a biological sample
Patent: US 6551778-A 38 22-APR-2003;
JOURNAL
FEATURES
source
1. .49
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 60.4%; Score 31.4; DB 6; Length 49;
Best Local Similarity 85.4%; Pred. No. 0.16; 6; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTG 41
2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

Db 2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

RESULT 13
AX025599 52 bp DNA linear PAT 16-SEP-2000
LOCUS
DEFINITION Sequence 78 from Patent WO0034517.
ACCESSION AX025599
VERSION AX025599.1 GI:10187267
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial construct
REFERENCE
1 Tan, P.S., van Maanen, C., Wagter, L.H., Schut, F., Brinkhof, J.M.,
Busing, H.Z. and Koopmans, H.H.
Detection of mycobacterium avium subspecies
Patent: WO 0034517-A 78 15-JUN-2000;
JOURNAL
GEZONDHEIDSDIENST VOOR DIEREN (NL) ; MAANEN CORNELIS VAN (NL) ; TAN
PARIS SOM TUWAN (NL) ; WAGTER LUCA HENDRIK ALBERT (NL) ;
MICROSCHEEN B V (NL) ; SCHUT FREDERIK (NL) ; BRINKHOF JOHANNES
MICHEL ANTH (NL) ; ENSING HENRIETTE ZWAANTJINA (NL) ; KOOPMANS
HENDRIK HIDDO (NL)

FEATURES
source
1. .52
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer-Primer reverse Mpnas798R"

ORIGIN
Query Match 60.4%; Score 31.4; DB 6; Length 52;
Best Local Similarity 85.4%; Pred. No. 0.16; 6; Indels 0; Gaps 0;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGCGCCCACTG 41
2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

Db 2 AATTATACGACTCACTATAGGAGACTGTGCTGACTG 42

RESULT 14
A99135 47 bp DNA linear PAT 26-JAN-2000
LOCUS
DEFINITION Sequence 9 from Patent WO9907898.
ACCESSION A99135
VERSION A99135.1 GI:6782088
KEYWORDS
SOURCE unidentified
ORGANISM unidentified

THIS PAGE BLANK (USE)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 00:19:57 ; Search time 343.065 Seconds
(without alignments)
643.920 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52
Sequence: 1 aattctatagactactat.....gcccaactgctaggatttc 52

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 3485926

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	52	100.0	52	6	ABK93891 Human Imm
2	36.4	70.0	50	5	AAf56540 HIV-1 det
3	36.4	70.0	50	6	ABK93893 Human Imm
4	36.4	70.0	51	5	AAf56558 HIV-1 det
5	36	69.2	53	2	AAV66330 Human Imm
6	36	69.2	54	2	AAQ86607 Human Imm
7	36	69.2	54	2	AAf15552 Human Imm
8	36	69.2	54	2	AAx23172 HIV regio
9	36	69.2	54	9	AAf56557 HIV-1 pro
10	31.8	61.2	52	6	ABK53107 HIV-1 pro
11	31.8	61.2	52	6	AAf45469 HIV-1 pro
12	31.4	60.4	49	3	AAf76206 Human pro
13	31.4	60.4	52	3	AAf63315 Mycobacte
14	31.2	60.0	47	2	AAx26214 Oligo com
15	31.2	60.0	47	9	AAf56491 PCR prime
16	31.1	59.6	48	2	AAf91790 Primer BB
17	31	59.6	48	2	AAf91790 Human Imm
18	30.4	58.5	52	2	AAQ86620 Human Imm
19	30.4	58.5	52	2	AAQ86639 Modified
20	30.4	58.5	52	2	AAf15575 Multiple
21	30.4	58.5	52	2	AAf15565 Human Imm
22	30.4	58.5	52	2	AAf42408 HIV probe
23	30.4	58.5	52	2	AAf66343 Human Imm

24	30.4	58.5	52	2	AAV66357 CML-2 chr
25	30.4	58.5	52	2	AAx23208 CML t(14;
26	30.4	58.5	52	2	AAx23185 HIV regio
27	30.4	58.5	52	2	AAf62570 Human Imm
28	30.2	58.1	50	6	ABK53105 HIV-1 gag
29	30.2	58.1	50	6	AAf45467 HIV-1 gag
30	30.2	58.1	53	6	ABK53137 HIV-1 pro
31	30.2	58.1	53	6	AAf45499 HIV-1 pro
32	29.8	57.3	48	2	AAf23689 Human pri
33	29.8	57.3	48	2	AAf58539 Human DNA
34	29.8	57.3	48	3	AAf7716 Human PRO
35	29.8	57.3	48	4	AAf97508 Human PRO
36	29.8	57.3	48	4	AAf93118 Human PRO
37	29.8	57.3	48	7	ABf57299 Primer p1
38	29.6	56.9	47	2	AAQ50478 Promoter-
39	29.6	56.9	47	2	AAQ57043 M. tuberc
40	29.6	56.9	47	2	AAf57024 WO923258
41	29.6	56.9	47	3	AAf89903 Amplifica
42	29.6	56.9	52	8	AAf43281 Nucleotid
43	29.4	56.5	47	2	AAf91784 Primer BB
44	29.4	56.5	51	6	ABf12953 Mycobacte
45	29.2	56.2	45	2	AAQ86640 Promoter-

ALIGNMENTS

RESULT 1
ABK93891
ID ABK93891 standard; DNA; 52 BP.
XX
AC ABK93891;
XX
DT 29-AUG-2003 (revised)
DT 26-AUG-2002 (first entry)
XX
DE Human immunodeficiency virus type 2 detection probe #15.
XX
KM Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;
KM hepatitis C virus; HCV; probe; ss.
XX
OS Human immunodeficiency virus 2.
XX
PN WO200234951-A2.
XX
PD 02-MAY-2002.
XX
PF 22-OCT-2001; 2001WO-US045396.
XX
PR 23-OCT-2000; 2000US-0242620P.
PR 30-MAR-2001; 2001US-028058P.
PA (GENP-) GEN-PROBE INC.
XX
PI Yang YV, Burrell TA;
XX
DR WPI; 2002-489953/52.
XX
PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
PT amplifying nucleic acids with oligonucleotides and detecting nucleic
PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
PT duplex.
XX
PS Claim 11; Page 25; 58pp; English.
XX
CC The invention relates to a method of detecting human immunodeficiency
CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
CC base sequence, and detecting the amplified NA; or providing a
CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
CC probe to form probe:target duplex, and detecting the duplex. The method
CC is useful for detecting the presence of HIV-2 NAs in a lysate or a blood
CC product such as plasma or serum, and also for detecting subtypes A, B, C

CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC in blood serum and also as components of multiplex amplification
 CC reactions that synthesize amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABR93877-ABR93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 52 BP; 15 A; 11 C; 13 G; 13 T; 0 U; 0 Other;

Query Match 100.0%; Score 52; DB 6; Length 52;
 Best Local Similarity 100.0%; Pred. No. 1.5e-12;
 Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 52
 DB 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 52

RESULT 2

ID AAF56540 standard; DNA; 50 BP.

AC AAF56540;

DT 11-SEP-2003 (revised)

DT 18-APR-2001 (first entry)

DE HIV-1 detection PCR primer SEQ ID NO: 8.

KM HIV-1 detection; diagnosis; blood screening; PCR primer; probe; ss.

OS Human immunodeficiency virus 1.

PN MO200104361-A2.

PD 18-JUN-2001.

PF 07-JUL-2000; 2000MO-US018685.

PR 09-JUL-1999; 99US-0143072P.

PA (GENP-) GEN-PROBE INC.

PA (BERG/) BEB G.G.

PA (YANG/) YANG Y.Y.

PA (KOLK/) KOLK D.P.

PA (GIAC/) GIACCHETTI C.

PA (MCDO/) MCDONOUGH S.H.

PI Bee CG, Yang Y.Y., Kolk D.P., Giachetti C., McDonough S.H.

DR WPI; 2001-147200/15.

PT Detecting HIV-1 nucleic acids in biological samples useful for diagnosing
 PT HIV-1 infection involves using nucleic acid capture oligomers,
 PT amplification oligomers and probe oligomers.

PS Claim 5; Page 50; 60pp; English.

CC The present invention provides probes and PCR primers for use in the
 CC detection of HIV-1. These are shown in AAF56533-AAF56589. They can be
 CC used to diagnose HIV infection and to ensure that blood and blood
 CC products do not contain the virus, thus enabling the prevention of HIV
 CC infection during blood transfusions. (Updated on 11-SEP-2003 to
 CC standardise OS field)

SQ Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 70.0%; Score 36.4; DB 5; Length 50;
 Best Local Similarity 94.2%; Pred. No. 8.6e-06;
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 52
 ID AAF56558 standard; DNA; 51 BP.

DB 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 50

RESULT 3

ID ABR93893 standard; DNA; 50 BP.

AC ABR93893;

DT 29-AUG-2003 (revised)

DT 26-AUG-2002 (first entry)

DE Human immunodeficiency virus type 2 detection probe #17.

KM Human immunodeficiency virus 2; HIV-2; HIV-1; hepatitis B virus; HBV;

KW hepatitis C virus; HCV; probe; ss.

OS Human immunodeficiency virus 2.

PN MO200234951-A2.

PD 02-MAY-2002.

PF 22-OCT-2001; 2001MO-US045396.

PR 23-OCT-2000; 2000US-0242620P.

PR 30-MAR-2001; 2001US-0280058P.

PA (GENP-) GEN-PROBE INC.

PI Yang Y.Y., Burrell T.A.

DR WPI; 2002-489953/52.

PT Detecting human immunodeficiency virus-2 nucleic acids in a sample, by
 PT amplifying nucleic acids with oligonucleotides and detecting nucleic
 PT acid, or hybridizing nucleic acid with a probe and detecting probe:target
 PT duplex.

PS Claim 11; Page 25; 58pp; English.

CC The invention relates to a method of detecting human immunodeficiency
 CC virus-2 nucleic acids (NA) in a biological sample, by contacting NAs with
 CC 1st and 2nd amplification oligonucleotides, amplifying HIV-2 nucleotide
 CC base sequence, and detecting the amplified NA, or providing a
 CC hybridisation probe and detectable label, hybridising HIV-2 NA with the
 CC probe to form probe:target duplex, and detecting the duplex. The method
 CC is useful for detecting the presence of HIV-2 NA in a lysate or a blood
 CC product such as plasma or serum, and also for detecting subtypes A, B, C
 CC and D of HIV-2. The method is useful for amplifying and detecting the NA
 CC reactions that synthesize amplicons corresponding to polynucleotides of
 CC unrelated viruses, e.g. HIV-1, hepatitis B virus (HBV) and hepatitis C
 CC virus (HCV). ABR93877-ABR93910 represent HIV-2 detection probes of the
 CC invention. (Updated on 29-AUG-2003 to standardise OS field)

SQ Sequence 50 BP; 15 A; 10 C; 12 G; 13 T; 0 U; 0 Other;

Query Match 70.0%; Score 36.4; DB 6; Length 50;
 Best Local Similarity 94.2%; Pred. No. 8.6e-06;
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

QY 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 52
 DB 1 AATTATATAGACTACTATAGGAGACGGGCGCCACCTGCTAGGATTTT 50

RESULT 4

ID AAF56558 standard; DNA; 51 BP.

AC AAF56558;

DT 11-SEP-2003 (revised)
 DT 18-APR-2001 (first entry)
 XX
 DE HIV-1 detection PCR primer SEQ ID NO: 26.
 XX
 KM HIV-1 detection; diagnosis; blood screening; PCR primer; probe; ss.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN W0200104361-A2.
 XX
 PD 18-JAN-2001.
 XX
 PF 07-JUL-2000; 2000WO-US018685.
 XX
 PR 09-JUL-1999; 99US-0143072P.
 XX
 PA (GENP-) GEN-PROBE INC.
 PA (BEEG/) BEE G G.
 PA (YANG/) YANG Y Y.
 PA (KOLK/) KOLK D P.
 PA (GIAC/) GIACHETTI C.
 PA (MCDON/) MCDONOUGH S H.
 PI Bee GG, Yang YV, Kolk DP, Giachetti C, McDonough SH;
 XX
 DR WPI; 2001-147200/15.
 XX
 PT Detecting HIV-1 nucleic acids in biological samples useful for diagnosing
 PT HIV-1 infection involves using nucleic acid capture oligomers,
 PT amplification oligomers and probe oligomers.
 XX
 PS Claim 5; Page 54; 60pp; English.
 XX
 CC The present invention provides probes and PCR primers for use in the
 CC detection of HIV-1. These are shown in AAF56533-AAF56589. They can be
 CC used to diagnose HIV infection and to ensure that blood and blood
 CC products do not contain the virus, thus enabling the prevention of HIV
 CC infection during blood transfusions. (Updated on 11-SEP-2003 to
 CC standardise OS field)
 CC
 SQ Sequence 51 BP; 15 A; 11 C; 12 G; 13 T; 0 U; 0 Other;
 XX
 Query Match 70.0%; Score 36.4; DB 5; Length 51;
 Best Local Similarity 94.2%; Pred. No. 8.6e-06;
 Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
 QY 1 AATTATACGACTCATTATAGGAGACGGGCGCCCAACTGCTAGGATTTT 52
 Db 1 AATTATACGACTCATTATAGGAGACGGGCGCCCA--CTGCTAGGATTTT 50
 XX
 RESULT 5
 AAV66330
 ID AAV66330 standard; DNA; 53 BP.
 XX
 AC AAV66330;
 XX
 DT 06-JAN-1999 (first entry)
 XX
 DE Human immunodeficiency virus region 1 (+) primer.
 XX
 KM Region 1; block splice template; autocatalytic RNA amplification; primer;
 KM ss.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus.
 XX
 PN US5824518-A.
 XX
 PD 20-OCT-1998.
 XX
 PF 06-JUN-1995; 95US-00469067.

XX
 PR 11-JUL-1989; 89US-00379501.
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1998-582557/49.
 XX
 PT Block splice template useful for amplification of nucleic acids -
 PT comprises two nucleic acid regions, the first region located 3' of the
 PT second region and blocked at its 3' terminus to inhibit primer extension
 PT by a DNA polymerase.
 XX
 PS Disclosure; Col 9; 51pp; English.
 XX
 CC AAV66330-31 represent Human immunodeficiency virus region 1 primers. The
 CC primers are used to exemplify the invention, together with probe
 CC AAV66332. The specification describes methods of synthesising multiple
 CC copies of a target nucleic acid sequence autocatalytically under
 CC conditions of substantially constant temperature, ionic strength and pH
 CC are provided in which multiple RNA copies of the target sequence
 CC autocatalytically generate additional copies. The target sequence is a
 CC block splice template which comprises two nucleic acid regions. The first
 CC region is located 3' of the second region and is blocked at its 3'
 CC terminus to inhibit primer extension by a DNA polymerase, and the second
 CC region comprises a promoter sequence recognised by an RNA polymerase. The
 CC methods are used to amplify nucleic acids, especially RNA, for analysis,
 CC cloning or probe production
 XX
 SQ Sequence 53 BP; 15 A; 11 C; 13 G; 14 T; 0 U; 0 Other;
 XX
 Query Match 69.2%; Score 36; DB 2; Length 53;
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 1 AATTATACGACTCATTATAGGAGACGGGCGCCCAACTGCTAGGATTTT 52
 Db 1 AATTATACGACTCATTATAGGAGACGAGCAAGGACTTCCGCTGGGACTTT 52
 XX
 RESULT 6
 AAQ86607
 ID AAQ86607 standard; DNA; 54 BP.
 XX
 AC AAQ86607;
 XX
 DT 25-MAR-2003 (revised)
 DT 15-NOV-1995 (first entry)
 XX
 DE Human immunodeficiency virus (HIV) region 1 plus strand primer.
 XX
 KM Primer; autocatalytic; target; HIV; ss.
 XX
 OS Synthetic.
 XX
 PN US5399491-A.
 XX
 PD 21-MAR-1995.
 XX
 PF 19-MAR-1992; 92US-00855732.
 XX
 PR 11-JUL-1989; 89US-00379501.
 PR 10-JUL-1990; 90US-00550837.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Fultz TJ, Kacian DL;
 XX
 DR WPI; 1995-130686/17.
 XX
 PT Amplification of nucleic acid targets - using a reverse transcriptase

PT with RNase H activity and a RNA polymerase at constant temp.
 XX
 PS Disclosure; Col 9; 58pp; English.
 XX

CC AA086607-09 are primers and a probe for the human immunodeficiency virus
 CC region 1. They are used to produce autocatalytic oligonucleotides which
 CC require no change in the experimental conditions i.e. constant
 CC temperature, pH and ionic strength. These sequences are useful in
 CC generating multiple copies of specific nucleic acid target sequences.
 CC (Updated on 25-MAR-2003 to correct PF field.)
 XX

SQ Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AATTTAATACGACTCTATAGGAGACGGCGCCAACTGCTAGGATTTT 52
 DB 1 AATTTAATACGACTCTATAGGAGACGACAAAGGACTTTCCGCTGGGACTTT 52

RESULT 7

AAT15552
 ID AAT15552 standard; DNA; 54 BP.

XX AAT15552;

AC 25-MAR-2003 (revised)
 DT 16-JUL-1996 (first entry)

XX Human immunodeficiency virus (HIV) region 1 (+) primer.

KW Human immunodeficiency virus; HIV; region 1; primer; auto-catalytic;
 KM synthesis; RNA target sequence; assay; detection; quantification; ss.
 XX Synthetic.

OS US5480784-A.

PN 02-JAN-1996.

PD 10-JUL-1990; 90US-00550837.

PF 11-JUL-1989; 89US-00379501.

PR (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

PS WPI; 1996-068248/07.

XX The present sequence is a primer for the human immunodeficiency virus
 XX region 1, which was used to demonstrate an improved method for
 XX synthesizing multiple copies of a RNA target sequence. The method
 XX comprises combining the target with a primer which hybridizes to the 3'-
 XX terminal portion of the target, a promoter primer which hybridizes with a
 XX portion of the DNA primer extension prod., reverse transcriptase, RNase H
 XX and/or transcriptase. It can be used as a component of an assay to detect
 XX forensic samples. It also has the advantages of being autocatalytic,
 XX using the cooperative action of a DNA polymerase, e.g. a reverse
 XX transcriptase and avoids repetitive manipulations of reaction conditions,
 XX e.g. temp., ionic strength and pH. (Updated on 25-MAR-2003 to correct PF
 XX field.)

Example; Col 9-10; 51pp; English.

SQ Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AATTTAATACGACTCTATAGGAGACGGCGCCAACTGCTAGGATTTT 52
 DB 1 AATTTAATACGACTCTATAGGAGACGACAAAGGACTTTCCGCTGGGACTTT 52

RESULT 8

AAX23172
 ID AAX23172 standard; DNA; 54 BP.

XX AAX23172;

AC 11-JUN-1999 (first entry)

DE HIV region 1 primer #1.

KW Autocatalytic amplification; transcription-based amplification;
 KM thermal cycling; diagnostic; environmental testing; probe; detection;
 XX genetic disease; infectious disease; microorganism; food; forensic;
 XX paternity; primer; ss.

OS Synthetic.

PN US5888779-A.

PD 30-MAR-1999.

PF 05-JUN-1995; 95US-00461654.

PR 11-JUL-1989; 89US-00379501.

PR 10-JUL-1990; 90US-00550837.

PA (GENP-) GEN-PROBE INC.

PI Fultz TJ, Kacian DL;

PS WPI; 1999-253231/21.

XX Kit for autocatalytic amplification of RNA targets.

XX Disclosure; Col 9; 51pp; English.

XX This invention describes a novel method for the autocatalytic
 XX amplification of an RNA target in a transcription-based amplification
 XX system without thermal cycling. The method generates oligonucleotides for
 XX diagnostic or environmental testing, for use e.g. as probes and in
 XX cloning. Typical applications are the detection of genetic or infectious
 XX diseases, the monitoring of responses to therapy, the quantitation or
 XX detection of microorganisms in foods, forensic studies and the
 XX establishment of paternity. Kits containing the products of the invention
 XX provide many copies of selected RNA targets under conditions of constant
 XX temperature, ionic strength and pH. Specific amplification of RNA targets
 XX increases sensitivity, convenience, accuracy and the reliability of
 XX assays

SQ Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 69.2%; Score 36; DB 2; Length 54;
 Best Local Similarity 80.8%; Pred. No. 1.3e-05;
 Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 AATTTAATACGACTCTATAGGAGACGGCGCCAACTGCTAGGATTTT 52
 DB 1 AATTTAATACGACTCTATAGGAGACGACAAAGGACTTTCCGCTGGGACTTT 52

RESULT 9

AAD62557
ID AAD62557 standard; DNA; 54 BP.
XX
AC AAD62557;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human immunodeficiency virus (HIV) region 1 specific PCR primer #1.
XX
KM Amplification; human immunodeficiency virus; environmental testing; HIV;
KM detection; diagnostic testing; PCR; primer; ss.
XX
OS Human immunodeficiency virus.
XX
PN US6589734-B1.
XX
PD 08-JUL-2003.
XX
PF 08-OCT-1998; 98US-00168947.
XX
PR 11-JUL-1989; 89US-00379501.
PR 10-JUL-1990; 90US-00550837.
PR 06-JUN-1995; 95US-00469067.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Kacian DL, Fultz TJ, McDonough SH;
XX
DR WPI; 2003-810379/76.
XX
PT New oligonucleotide probe, useful in detecting HIV nucleic acid in a
PT sample and for environmental and diagnostic testing.
XX
PS Claim 13; Col 9; 62pp; English.
XX
CC The invention relates to oligonucleotides useful in amplifying and
CC detecting human immunodeficiency virus (HIV) nucleic acid in a sample.
CC The invention is used for environmental testing, diagnostic testing,
CC research studies and for the preparation of reagents or materials for
CC cloning or other purposes. The present sequence is HIV region specific
CC PCR primer. This sequence is used in the invention
XX
SQ Sequence 54 BP; 15 A; 12 C; 13 G; 14 T; 0 U; 0 Other;
XX
Query Match 69.2%; Score 36; DB 9; Length 54;
Best Local Similarity 80.8%; Pred. No. 1.3e-05;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
OY 1 AATTATAGACCTACTATAGGAGACGGCGCCACCTGCTAGGATTT 52
DB 1 AATTATAGACCTACTATAGGAGACGACGACTTTCGCGGAGACTTT 52
RESULT 10
ABK3107
ID ABK3107 standard; DNA; 52 BP.
XX
AC ABK3107;
XX
DT 29-AUG-2003 (revised)
DT 12-AUG-2002 (first entry)
XX
DE HIV-1 protease gene specific oligonucleotide primer #1.
XX
KM HIV; human immunodeficiency virus; ss; primer; gag; pol; protease;
KM reverse transcriptase; infection; PCR.
XX
OS Human immunodeficiency virus 1.
XX
PN US2002055095-A1.
XX
PD 09-MAY-2002.
XX

PF 31-AUG-2001; 2001US-00944036.
XX
XX 01-SEP-2000; 2000US-0229790P.
XX
XX (YANG/) YANG Y Y.
PA (BREN/) BRENTANO S T.
PA (BABO/) BABOLA O.
PA (TRAN/) TRAN N.
PA (VERN/) VERNET G.
XX
PI Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
XX
XX WPI; 2002-462902/49.
XX
DR New nucleic acid oligomers for amplifying a nucleotide sequence from HIV-
PT 1 and probes for detecting the amplified product are specific for gag and
PT pol regions and are useful to detect different subtypes of HIV-1.
XX
PS Claim 1; Page 14; 37pp; English.
XX
XX This invention relates to a series of nucleic acid oligomers for
CC amplifying and detecting a nucleotide sequence of human immunodeficiency
CC virus type 1 (HIV-1). The invention also comprises a labeled
CC oligonucleotide that specifically hybridizes to an HIV-1 sequence derived
CC from gag or pol sequences, having one of the sequences fully defined in
CC the specification, and a method for detecting HIV-1 in a biological
CC sample, comprising mixing the sample with two or more of the
CC amplification oligomers that specifically amplify at least one HIV-1
CC target sequence within gag and a pol sequence which is a protease or
CC reverse transcriptase sequence, amplifying the target, and detecting the
CC amplified product. The oligonucleotides of the invention may be used to
CC diagnose HIV-1 infection. The presents sequence represents a PCR primer
CC used to amplify the HIV-1 protease gene in the HIV detection method of
CC the invention. (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 52 BP; 16 A; 14 C; 8 G; 14 T; 0 U; 0 Other;
XX
Query Match 61.2%; Score 31.8; DB 6; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.00085;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
OY 1 AATTATAGACCTACTATAGGAGACGGCGCCACCTGCTAGGATTT 51
DB 1 AATTATAGACCTACTATAGGAGACGACGACATCCATCCTCGCTTT 51
RESULT 11
AAL45469
ID AAL45469 standard; DNA; 52 BP.
XX
AC AAL45469;
XX
DT 29-AUG-2003 (revised)
DT 06-JUN-2002 (first entry)
XX
DE HIV-1 pol gene protease amplification oligomer SEQ ID NO: 7.
XX
KM HIV-1; gag gene; pol gene; PCR; primer; drug resistance; genetic subtype;
KM probe; ss.
XX
OS Human immunodeficiency virus 1.
OS Enterobacteria phage T7.
XX
PN WO200220852-A1.
XX
PD 14-MAR-2002.
XX
PF 01-SEP-2000; 2000WO-US024117.
XX
PR 01-SEP-2000; 2000WO-US024117.
XX
PA (GENP-) GEN-PROBE INC.
PA (INMR) BIOMERIEUX SA.

XX Yang YY, Brentano ST, Babola O, Tran N, Vernet G;
 XX WPI; 2002-292273/33.
 DR
 XX
 PT New nucleic acid oligomer, useful for detecting selected regions of gag
 PT and pol genes of human immune deficiency virus, particularly for
 XX assessing drug resistance.
 XX
 PS Claim 1; Page 38; 82pp; English.
 CC The present invention provides a number of nucleic acid oligomers which
 CC can be used to amplify the gag and pol genes of human immunodeficiency
 CC virus type 1 (HIV-1). These are used to detect regions of the gag and pol
 CC genes, especially regions associated with drug resistance, and also for
 CC identifying genetic subtypes of the virus. The present sequence is an
 CC oligomer of the invention. (Updated on 29-AUG-2003 to standardise OS
 CC field)
 CC
 SQ Sequence 52 BP; 16 A; 14 C; 8 G; 14 T; 0 U; 0 Other;
 Query Match 61.2%; Score 31.8; DB 6; Length 52;
 Best Local Similarity 76.5%; Pred. No. 0.00085;
 Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
 QY 1 AATTATAGACTCTATAGGAGACGGGCGCCAACTGCTGATTT 51
 Db 1 AATTATAGACTCTATAGGAGACGGGCGCCAACTGCTGATTT 51
 RESULT 12
 ID AAA76206 standard; DNA; 49 BP.
 XX AAA76206;
 AC
 XX
 DT 25-JUN-2001 (first entry)
 XX
 DE Human prostate specific antigen PCR primer SEQ ID NO: 35.
 XX
 KW Prostate specific antigen; PSA; prostate-specific membrane antigen; PSMA;
 KW glandular kallikrein-2; hK2; prostate cancer; breast cancer; probe;
 XX PCR primer; ss.
 OS Homo sapiens.
 XX
 PN WO20044940-A2.
 XX
 PD 03-AUG-2000.
 XX
 PF 28-JAN-2000; 2000WO-US002270.
 XX
 PR 28-JAN-1999; 99US-0117640P.
 XX
 PA (GENP-) GEN-PROBE INC.
 XX
 PI Harvey RC, Clark TJ;
 XX
 DR WPI; 2000-505986/45.
 XX
 PT Detecting prostate-specific antigen (PSA) prostate specific membrane
 PT antigen (PSMA) or human kallikrein 2 (hK2) nucleic acids in samples using
 PT probe molecules, useful for the diagnosis of prostate and breast cancers.
 XX
 PS Claim 1; Page 13; 77pp; English.
 CC The present invention is concerned with the detection of nucleic acid
 CC markers for prostate and breast cancer, and PCR primers and probes which
 CC are able to detect and quantify these markers. Prostate specific antigen
 CC (PSA), prostate-specific membrane antigen (PSMA) and glandular kallikrein
 CC -2 (hK2) have all been linked to prostate and breast cancer, and the
 CC primers and probes of the invention are able to detect the abnormal
 CC presence of mRNA expressed by their coding sequences in tissues other

CC than the prostate. This enables the presence of cancer to be perceived
 CC and aids in the detection of metastases
 XX
 SQ Sequence 49 BP; 17 A; 10 C; 10 G; 12 T; 0 U; 0 Other;
 Query Match 60.4%; Score 31.4; DB 3; Length 49;
 Best Local Similarity 85.4%; Pred. No. 0.0012;
 Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATTATAGACTCTATAGGAGACGGGCGCCAACTG 41
 Db 2 AATTATAGACTCTATAGGAGACGGGCGCCAACTG 42
 RESULT 13
 ID AAA63315 standard; DNA; 52 BP.
 XX AAA63315;
 AC
 XX
 DT 15-FEB-2001 (first entry)
 XX
 DE Mycobacterium avium paratuberculosis 23S gene PCR primer MPas798R.
 XX
 KW Johne's disease; Crohn's disease; subspecies detection; 23S rRNA;
 KW PCR primer; ss.
 XX
 OS Mycobacterium avium subsp. paratuberculosis.
 XX
 PN WO200034517-A1.
 XX
 PD 15-JUN-2000.
 XX
 PF 03-DEC-1999; 99WO-NL000741.
 XX
 PR 04-DEC-1998; 98EP-00204117.
 XX
 PA (MICR-) MICROSCREEN BV.
 PA (GEZO-) GEZONDHEIDSDIENST DIEREN.
 XX
 PI Schut F, Ensing HZ, Koopmans HH, Tan PST, Wagter LHA,
 PI Brinkhof JMA, Van Maanen C;
 XX
 DR WPI; 2000-423446/36.
 XX
 PT Detection of Mycobacterium avium paratuberculosis by identification of
 PT specific 23S rRNA mutations at positions 754, 1363 or 3093 useful for
 PT diagnosis of Johne's disease.
 XX
 PS Example 1; Fig 6; 81pp; English.
 CC The present sequence is a PCR primer used in the amplification of the
 CC Mycobacterium avium subsp. paratuberculosis 23S rRNA gene. This gene
 CC contains several mutations when compared to other Mycobacterium avium
 CC subspecies, and some are unique enough to allow the development of a
 CC probe which enables specific identification of the presence of
 CC paratuberculosis. The organism is responsible for Johne's disease in
 CC ruminants, especially cows, and is possibly transmitted to humans where
 CC it may lead to Crohn's disease. Efficient detection of the bacterium,
 CC using a probe designed using this sequence, can be used to identify
 CC infected animals so that they can be removed from the herd and destroyed
 CC
 SQ Sequence 52 BP; 15 A; 12 C; 13 G; 12 T; 0 U; 0 Other;
 Query Match 60.4%; Score 31.4; DB 3; Length 52;
 Best Local Similarity 85.4%; Pred. No. 0.0013;
 Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 AATTATAGACTCTATAGGAGACGGGCGCCAACTG 41
 Db 2 AATTATAGACTCTATAGGAGACGGGCGCCAACTG 42

```

RESULT 14
AXX26214
ID AAX26214 standard; DNA; 47 BP.
XX
AC AAX26214;
XX
DT 21-MAY-1999 (first entry)
XX
DE Oligo complementary to LTR region of HIV-1 genome.
XX
KM HIV-1; nucleic acid amplification; detection; LTR; primer; probe;
XX human immunodeficiency virus type 1; long terminal repeat; ss.
XX
OS Synthetic.
XX Human immunodeficiency virus 1.
XX
PN WO9907898-A1.
XX
PD 18-FEB-1999.
XX
PF 05-AUG-1998; 98MO-EP004945.
XX
PR 08-AUG-1997; 97EP-00202455.
XX
PA (ALKU) AKZO NOBEL NV.
XX
PI Goudenit J, Oudshoorn P, Jurrians S, Lukashov VV;
XX
DR WPI; 1999-167457/14.
XX
PT New oligonucleotide primers and probes complementary to the LTR region of
XX HIV-1 - useful for amplification and detection of HIV-1 infections.
XX
PS Claim 2; Page 23; 30pp; English.
XX
CC Sequences AAX26206 to AAX26217 represent claimed oligonucleotides that
XX can be used as primers and probes in the amplification and detection of
XX all subtypes of human immunodeficiency virus type 1 (HIV-1). The oligos
XX are substantially complementary to a sequence of the long terminal repeat
XX (LTR) region of a nucleic acid sequence of a HIV genome. The invention
XX provides a method for detection of HIV-1 nucleic acid using these
XX sequences. Unlike prior art primers and probes, these oligos can detect
XX all known subtypes of HIV-1 with high sensitivity and accuracy
XX
SQ Sequence 47 BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
Query Match 60.0%; Score 31.2; DB 2; Length 47;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATTATAGCACTACTATAGGAGACGGGCGCCA 36
Db 2 ATTCTAATACGACTACTATAGGAGAGGGGCGCCA 37

```

```

RESULT 15
ADB48105
ID ADB48105 standard; DNA; 47 BP.
XX
AC ADB48105;
XX
DT 29-JAN-2004 (first entry)
XX
DE Primer #1 of the invention.
XX
KM retroviral nucleic acid; body fluid; primer; ss.
XX
OS Synthetic.
XX
PN WO2003080869-A2.
XX
PD 02-OCT-2003.
XX

```

```

PF 03-JUL-2003; 2003MO-NL000491.
XX
PR 04-JUL-2002; 2002EP-00077697.
XX
PA (PRIM-) PRIMAGEN HOLDING BV.
XX
PI De Rooij ER, De Baar MP;
XX
DR WPI; 2003-876928/81.
XX
KM Detecting and quantifying a nucleic acid in a sample, useful for
XX detecting viral RNA, comprises administering the sample to a carrier, and
XX exposing the carrier to nucleic acid isolation solution to extract an
XX amount of nucleic acid.
XX
PS Example 1; SEQ ID NO 1; 30pp; English.
XX
CC The present invention relates to detecting and quantifying a nucleic acid
XX in at least one sample comprising administering the sample to a solid
XX carrier capable of at least in part absorbing the sample and providing at
XX least a representative part of the carrier to a nucleic acid isolation
XX solution to extract a representative amount of the nucleic acid from the
XX carrier. The method is particularly useful for detecting viral nucleic
XX acid, especially retroviral nucleic acid, in a sample such as a body
XX fluid. The present sequence represents a primer of the invention.
XX
SQ Sequence 47 BP; 15 A; 10 C; 13 G; 9 T; 0 U; 0 Other;
Query Match 60.0%; Score 31.2; DB 9; Length 47;
Best Local Similarity 91.7%; Pred. No. 0.0015;
Matches 33; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 AATTATAGCACTACTATAGGAGACGGGCGCCA 36
Db 2 ATTCTAATACGACTACTATAGGAGAGGGGCGCCA 37

```

Search completed: August 31, 2004, 01:37.13
Job time : 345.065 secs

THIS PAGE BLANK (CONT)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:14:18 ; Search time 2634.44 Seconds
(without alignments)
589.436 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52

Sequence: 1 aacttaatacagactcaactat.....gcccaactgctagsgatttc 52

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 569298

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

EST.*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estm:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	26	50.0	79	9	AJ282930 4A3A-PIE1
2	25.6	49.2	100	9	AJ353756 zeh0940.8
3	25.6	49.2	100	29	CG728851 1119104C1
4	25.4	48.8	87	14	CA406952 1003101 H

5	25.4	48.8	90	29	CG732206	CG732206 1119146G0
6	25.2	47.5	98	29	CG729102	CG729102 1119107G0
7	24.6	47.3	96	9	A1616894	A1616894 zeh0783.
8	23.8	45.8	75	9	A1087772	A1087772 SKORAMCAQ
9	23.8	45.8	79	14	CA336070	CA336070 NISC_1u07
10	23.6	45.4	86	29	CG733887	CG733887 1119160E1
11	23.6	45.4	90	29	CG732908	CG732908 1119152D0
12	23.6	45.4	95	9	A1353162	A1353162 zeh0113.8
13	23.6	45.4	95	9	A1353583	A1353583 zeh0701.8
14	23.6	45.4	96	9	A1617314	A1617314 zeh11351.
15	23.6	45.4	96	10	AW455598	AW455598 zeh11725
16	23.6	45.4	100	29	CG729011	CG729011 1119106D0
17	23.6	45.4	100	29	CG729055	CG729055 1119107A0
18	23.4	45.0	76	14	CF651968	CF651968 26-L02013
19	23.3	44.2	30	28	AO797214	AO797214 RPCI-22-4
20	22.8	43.8	55	14	CB261880	CB261880 83-E8880-
21	22.8	43.8	96	14	R29179	R29179 F1-287D 22
22	22.4	43.1	86	29	CG807118	CG807118 1118077H0
23	22.4	43.1	88	29	CG728803	CG728803 1119103C1
24	22.4	43.1	89	14	N88337	N88337 K3123P Huma
25	22.4	43.1	97	9	AA051807	AA051807 SWAMCA143
26	22.4	43.1	100	29	CG728814	CG728814 1119103E1
27	22.4	43.1	100	29	CG729247	CG729247 1119110B0
28	22.4	43.1	100	29	CG731464	CG731464 1119140G1
29	22.4	43.1	100	29	CG732356	CG732356 1119147G1
30	22.2	42.7	51	14	CD005157	CD005157 VVB049D11
31	22.2	42.7	54	29	CG807965	CG807965 1118088C1
32	22.2	42.7	55	14	CB263019	CB263019 38-E8881-
33	22.2	42.7	61	13	BU634607	BU634607 009H07 In
34	22.2	42.7	66	14	CD288815	CD288815 7 N19. abd
35	22.2	42.7	72	29	CG731440	CG731440 1119140E1
36	22.2	42.7	73	9	AA680645	AA680645 LmfPrAm09
37	22.2	42.7	77	13	BU634641	BU634641 012F12 In
38	22.2	42.7	78	29	CG732916	CG732916 1119152F0
39	22.2	42.7	78	29	CG799906	CG799906 1118005B0
40	22.2	42.7	80	9	AJ494595	AJ494595 AJ494595
41	22.2	42.7	80	14	CB262186	CB262186 71-E8724-
42	22.2	42.7	86	29	CG799851	CG799851 1118005B0
43	22.2	42.7	86	29	CG807595	CG807595 1118005B1
44	22.2	42.7	87	14	CF200277	CF200277 G1T1279 R
45	22.2	42.7	87	29	CG729167	CG729167 1119108G0

ALIGNMENTS

RESULT 1
AJ282930 79 bp mRNA linear EST 30-JUN-2000
LOCUS 4A3A-PIE1-R Anopheles gambiae immune competent 4A3A Anopheles
DEFINITION gambiae CDNA clone 4A3A-PIE1, mRNA sequence.
ACCESSION AJ282930 GI:6930809
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT
Contact: Dimopoulos G
Fotis C. Kafatos laboratory
European Molecular Biology Laboratory
Meyerothofstrasse 1, 69117 Heidelberg, Germany.

FEATURES

Location/Qualifiers

1..79
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="4a r/r"
/db_xref="taxon:7165"
/clone="4A3A-PIE1"
/cell_line="immune competent 4A3A"
/lab_host="E. coli DH10B"
/note="Vector: pTZ19-Pac (Pharmacia) with a modified polylinker Site_1: EcoRI; Site 2: NotI; sequenced from forward priming site which reads from the 3' end of the cDNA. The 4A3A is a directionally cloned and normalized cDNA library that was constructed from the 4A3A cell line oligo-T primed cDNA according to: Bonaldi, Lennon & Soares (1996) : Normalization and Subtraction: Two approaches To Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN

Query Match 50.0%; Score 26; DB 9; Length 79;
Best Local Similarity 85.3%; Pred. No. 13;
Matches 29; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCC 34
28 AATTATACGACTCACTATAGGAGATTGGCCCC 61

RESULT 2 100 bp mRNA linear EST 04-JAN-1999
A1353756 zeh0940.seq.F Zebrafish Embryonic Heart cDNA library Danilo rerio
LOCUS A1353756 cDNA 5' mRNA sequence.
ACCESSION A1353756
KEYWORDS A1353756.1 GI:4093909
SOURCE EST.
ORGANISM Danilo rerio (zebrafish)
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Osteichthyes;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 100)
Tom,C., Mabiy,J.D., Dempsey,A.A., Hwang,D.M., Fishman,M.C. and
Liew,C.C.
Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cliw@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAGCTCGAATTAACCTCACTAAAGG 3'
BACKWARD: 5' CCAATTAATGTAATGCTCACTAAAGG 3'
Seq primer: 5' GAAATTAACCTCACTAAAGG 3'.
Location/Qualifiers
1..100
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue MRF"
/clone_lib="zebrafish Embryonic Heart cDNA library"
/note="Organ: heart; Vector: lambda ZAP Express; Site_1:
EcoRI; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP

ORIGIN

Express vector. "

Query Match 49.2%; Score 25.6; DB 9; Length 100;
Best Local Similarity 70.8%; Pred. No. 20;
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCCACCTGTAAGGA 48
98 AATTATACGACTCACTATAGGAGCAATTGGGTACACTTACCTGTA 51

RESULT 3

CG728851 100 bp DNA linear GSS 20-OCT-2003
1119104C10.1EL_x1 1119 - Rescuemu Grid AA Zea mays genomic, genomic
survey sequence.
CG728851
ACCESSION CG728851.1 GI:37769986
VERSION GSS.
KEYWORDS Zea mays
SOURCE Zea mays
ORGANISM Zea mays
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
1 (bases 1 to 100)
Walbot,V.
Maize genomic sequences found using engineered Rescuemu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119104 row: 12
Classes: transposon-tagged.
Location/Qualifiers
1..100
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - Rescuemu Grid AA"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site_1: BamHI; Site 2: BglII;
Rescuemu is a 4.9 Kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic
Mu elements insert preferentially into transcrip-
tion units. For more information on Rescuemu, go to the web
site 'www.zmdb.jasrate.edu' and follow the links for
'Rescuemu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

Location/Qualifiers

1..100
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - Rescuemu Grid AA"
/note="Organ: leaf; Vector: Rescuemu (engineered from
pBluescript backbone); Site_1: BamHI; Site 2: BglII;
Rescuemu is a 4.9 Kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic
Mu elements insert preferentially into transcrip-
tion units. For more information on Rescuemu, go to the web
site 'www.zmdb.jasrate.edu' and follow the links for
'Rescuemu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN

Query Match 49.2%; Score 25.6; DB 29; Length 100;
Best Local Similarity 70.8%; Pred. No. 20;
Matches 34; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGACGGCGCCACCTGTAAGGA 48
29 AATTATACGACTCACTATAGGAGCAATTGGCGGAGACGGCGGTGA 76

```

RESULT 4
CA406952/c      87 bp      mRNA      linear      EST 07-NOV-2002
LOCUS           1003101 Human Fat Cell 5'-Stretch Plus cDNA Library Homo sapiens
DEFINITION      CDNA 5', mRNA sequence.
ACCESSION       CA406952
VERSION         CA406952.1 GI:24771823
KEYWORDS        EST.
SOURCE          Homo sapiens (human)
ORGANISM        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS         Yang, R.-Z., Shuldiner, A. and Gong, D.-W.
TITLE           EST analysis of human adipose gene expression
JOURNAL         Unpublished (2002)
COMMENT         Contact: Gong Da-Wei
                  Division of Endocrinology, Diabetes and Nutrition
                  University of Maryland
                  660 Redwood St. HH497, Baltimore, MD 21201, USA
                  Tel: 410 706 1672
                  Fax: 410 706 1622
                  Email: dgong@medicine.umaryland.edu
PCR Primers     FORWARD: CTCGGGAGCGCGGCATTGTTGGT
                  BACKWARD: AATAGCACTCACTATAGGCGCAATTGG
Seq primer:      GTTGTATCCCGGATTC.
FEATURES
source
1. .87
   /organism="Homo sapiens"
   /mol_type="mRNA"
   /db_xref="taxon:9606"
   /sex="Male and Female"
   /tissue_type="Adipose"
   /clone_lib="Human Fat Cell 5'-Stretch Plus cDNA Library"
   /note="Vector: lambdaTriplex"

ORIGIN
Query Match      48.8%; Score 25.4; DB 14; Length 87;
Best Local Similarity 82.9%; Pred. No. 22;
Matches 29; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 3 TTTAATACGACTCACTATAGGAGAGCGGCGCCAA 37
Db 86 TTTAATACGACTCACTATAGGCGCAATTGGCCAA 52

RESULT 5
CG732206      90 bp      DNA      linear      GSS 20-OCT-2003
LOCUS           1119146G02.1EL.X1 1119 - Rescuenu Grid AA Zea mays genomic, genomic
DEFINITION      Survey sequence.
ACCESSION       CG732206
VERSION         CG732206.1 GI:37774698
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS         Walbot, V.
TITLE           Maize genomic sequences found using engineered Rescuenu transposon
JOURNAL         Unpublished (2001)
COMMENT         Contact: Walbot V
                  Department of Biological Sciences
                  Stanford University
                  855 California Ave, Palo Alto, CA 94304, USA
                  Tel: 650 723 2227
                  Fax: 650 725 8221
                  Email: walbot@stanford.edu
                  Very probable ligation site of ends cut by single endonuclease.
                  Reverse complemented post-ligation sequence from source sequence.

```

```

Plate: 1119146 column: 36
Class: transposon-tagged.
FEATURES
source
1. .90
   /organism="Zea mays"
   /mol_type="genomic DNA"
   /cultiivar="mixed background W23/A186/B73/K55"
   /db_xref="taxon:4577"
   /tissue_type="leaf"
   /dev_stage="adult"
   /lab_host="DH10B"
   /clone_lib="1119 - Rescuenu Grid AA"
   /note="Organ: leaf; Vector: Rescuenu (engineered from
pBuescript backbone); Site 1: BamHI; Site 2: BglII;
Rescuenu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescuenu, go to the web
site 'www.zmdb.laestate.edu' and follow the links for
'Rescuenu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

ORIGIN
Query Match      48.8%; Score 25.4; DB 29; Length 90;
Best Local Similarity 96.3%; Pred. No. 23;
Matches 26; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AATTTATACGACTCACTATAGGAGAGA 27
Db 19 AATTTATACGACTCACTATAGGCGCA 45

RESULT 6
CG729102      98 bp      DNA      linear      GSS 20-OCT-2003
LOCUS           1119107G02.1EL.X1 1119 - Rescuenu Grid AA Zea mays genomic, genomic
DEFINITION      Survey sequence.
ACCESSION       CG729102
VERSION         CG729102.1 GI:37770478
KEYWORDS        GSS.
SOURCE          Zea mays
ORGANISM        Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
REFERENCE
AUTHORS         Walbot, V.
TITLE           Maize genomic sequences found using engineered Rescuenu transposon
JOURNAL         Unpublished (2001)
COMMENT         Contact: Walbot V
                  Department of Biological Sciences
                  Stanford University
                  855 California Ave, Palo Alto, CA 94304, USA
                  Tel: 650 723 2227
                  Fax: 650 725 8221
                  Email: walbot@stanford.edu
                  Very probable ligation site of ends cut by single endonuclease.
                  Reverse complemented post-ligation sequence from source sequence.
                  Plate: 1119107 row: 3
                  Class: transposon-tagged.
FEATURES
source
1. .98
   /organism="Zea mays"
   /mol_type="genomic DNA"
   /cultiivar="mixed background W23/A186/B73/K55"
   /db_xref="taxon:4577"
   /tissue_type="leaf"
   /dev_stage="adult"
   /lab_host="DH10B"
   /clone_lib="1119 - Rescuenu Grid AA"

```

/note="Organ: leaf; Vector: RescuedMu (engineered from pBluescript backbone); Site 1: BamHI, Site 2: BglII; RescuedMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescuedMu, go to the web site 'www.zmbl.jastate.edu' and follow the links for 'RescuedMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 48.5%; Score 25.2; DB 29; Length 96;
Best Local Similarity 78.9%; Pred. No. 28;
Matches 30; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 AATTATAGACTCTATTAGGAGCGGCGCCAC 38
DB 27 ATTGTATAGACTACTATTAGGCGCATTTGCCGAGC 64

RESULT 7 96 bp mRNA linear EST 21-APR-1999
A1616894
LOCUS zehnd783.seq.F Zebrafish Embryonic Heart cDNA Library Danilo rerio
DEFINITION cDNA 5', mRNA sequence.
ACCESSION A1616894
VERSION A1616894.1 GI:4626061
KEYWORDS EST.
SOURCE Danilo rerio (zebrafish)
ORGANISM Danilo rerio

REFERENCE Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Osteichthys; Cypriniformes; Cyprinidae; Danilo.
1 (bases 1 to 96)
AUTHORS Ton, C., Mabry, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and Liew, C.C.
TITLE Identification and Characterization of Expressed Sequence Tags from an Embryonic Zebrafish Heart cDNA Library
JOURNAL Unpublished (1999)
COMMENT Contact: Liew CC
Birmingham and Women's Hospital
Harvard Medical School
75 Francis St., Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: cllawerice.bwh.harvard.edu

PCR Primers
FORWARD: 5' GCCAGCTCGAATTAACTCTACTTAAGG 3'
BACKWARD: 5' CCAATGATTTGATAGACTACTTAAGGCGC 3'
Seq primer: 5' GAATTAACTCTACTTAAGG 3'.
FEATURES
source
1..96
Location/Qualifiers
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/dev_stage="embryonic day 3 post-fertilization"
/lab_host="B.coli XL1-Blue mrf."
/clone_idb="zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: Lambda ZAP Express; Site 1: EcoRI, Site 2: XhoI; mRNA was purified from embryonic zebrafish hearts (3 day post-fertilization). cDNA was synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI adaptors were ligated, followed by digestion with XhoI, for directional cloning into pre-digested Lambda ZAP Express vector."

ORIGIN

Query Match 47.3%; Score 24.6; DB 9; Length 96;
Best Local Similarity 70.2%; Pred. No. 47;
Matches 33; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 2 AATTATAGACTCTATTAGGAGCGGCGCCAACTGTTAGGA 48
DB 96 ATTGTATAGACTACTATTAGGCGCAATTGGGTACTTACTCGTA 50

RESULT 8 75 bp mRNA linear EST 18-AUG-1998
A1087772
LOCUS SMOVAMCAQ02F02SK Onchocerca volvulus adult male cDNA
DEFINITION (SM99MUM-OVAM) Onchocerca volvulus cDNA clone SMOVAMCAQ02F02 5', mRNA sequence.
ACCESSION A1087772
VERSION A1087772.1 GI:3426748
KEYWORDS EST.
SOURCE Onchocerca volvulus
ORGANISM Onchocerca volvulus

REFERENCE Bukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidae; Onchocercidae; Onchocerca.
1 (bases 1 to 75)
AUTHORS Lizotte-Waniewski, M. and Williams, S.A.
TITLE Genes expressed in adult male stage of Onchocerca volvulus
JOURNAL Unpublished (1998)
COMMENT Contact: Steven A. Williams
Molecular Parasitology
Smith College Department of Biological Sciences
Department of Biological Sciences, Clark Science Center, Smith
College, Northampton, MA, 01063, USA
Tel: 4135853826
Fax: 4135853786
Email: genome@smith.edu
Seq primer: p1nuescript SK.
FEATURES
source
1..75
Location/Qualifiers
/organism="Onchocerca volvulus"
/mol_type="mRNA"
/db_xref="taxon:6282"
/clone="SMOVMCAQ02F02"
/sex="male"
/dev_stage="adult"
/lab_host="XL1-Blue MRF"
/clone_idb="Onchocerca volvulus adult male cDNA (SM99MUM-OVAM)"
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2: Xho I; Filarial nematode parasite of humans. Six adult male worms of Onchocerca volvulus were isolated from consenting patients and quick frozen. Adult male mRNA was converted to double-stranded cDNA using reverse transcriptase and oligo(dT) followed by RNase H and DNA pol I. The library has 2 x 10⁵ independent recombinants and the average insert size is ~1100bp. The library was constructed by Michelle Lizotte-Waniewski with worms provided by Dr. Sara Lustigman. The library is available from Dr. Steven A. Williams, email: genome@smith.edu."

ORIGIN

Query Match 45.8%; Score 23.8; DB 9; Length 75;
Best Local Similarity 92.6%; Pred. No. 87;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AATTATAGACTCTATTAGGAGGA 27
DB 67 AATTATAGACTCTATTAGGAGGA 41

RESULT 9 79 bp mRNA linear EST 04-NOV-2002
CA336070
LOCUS NISC.lu07h08.y1 COGENE 4AR (4EAR) Homo sapiens cDNA clone
DEFINITION IMAGE:5607422 5', mRNA sequence.
ACCESSION CA336070
VERSION CA336070.1 GI:24554168
KEYWORDS EST.

SOURCE
Homo sapiens (human)

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 79)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
Unpublished (1997)

COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.E. Consortium/LNL
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
info@image.llnl.gov
Plate: LHAM12408 row: P column: 15
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
1..79
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="5607422"
/tissue_type="anterior rhombomeres 1-4 (4 pooled)"
/dev_stage="embryo, 4 weeks postconception"
/lab_host="DH10B"
/clone_lib="COGENE 4AR (4EAR)"
/note="Vector: PAMPI; cDNA primed using oligo-dT primer,
directionally cloned into UDG sites of PAMPI. Size
selected for insert sizes ranging from 0.3-1.6 kb.
Normalized to Cot10. Primary library, non-emplified.
Library constructed by M. Lovett. For more information on
this library, please contact R. Tidwell (Washington
University) or visit the COGENE website at
<http://hg.wustl.edu/COGENE/>."

FEATURES
source

ORIGIN
Query Match 45.8%; Score 23.8; DB 14; Length 79;
Best Local Similarity 92.6%; Pred. No. 89;
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY
3 TTTAATACGACTCACTATAGGAGAGC 29
|||||
40 TTTAATACGACTCACTATAGGAGTGC 14

RESULT 10
CG733887 86 bp DNA linear GSS 20-OCT-2003
LOCUS 1119160B1.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic
DEFINITION Survey sequence.
ACCESSION CG733887
VERSION CG733887.1 GI:37776379
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 86)
Walbot, V.
Maize genomic sequences found using engineered Rescemu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES
source

ORIGIN
Query Match 45.4%; Score 23.6; DB 29; Length 86;
Best Local Similarity 76.3%; Pred. No. 11e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

CY
1 AATTATACGACTCACTATAGGAGCGGCCCAAC 38
|||||
15 AATTATACGACTCACTATAGGCGATTTCAGCAGC 52

RESULT 11
CG732908 90 bp DNA linear GSS 20-OCT-2003
LOCUS 1119152D09.1EL.X1 1119 - Rescemu Grid AA Zea mays genomic, genomic
DEFINITION Survey sequence.
ACCESSION CG732908
VERSION CG732908.1 GI:37775400
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 90)
Walbot, V.
Maize genomic sequences found using engineered Rescemu transposon
Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Very probable ligation site of ends cut by single endonuclease.
Reverse complemented post-ligation sequence from source sequence.
Plate: 1119152 row: 14
Class: transposon-tagged.
Location/Qualifiers
1..90
/organism="Zea mays"
/mol_type="genomic DNA"
/cultiivar="mixed background W23/A188/B73/K55"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1119 - Rescemu Grid AA"
/note="Organ: leaf; Vector: Rescemu (engineered from
pBlueScript backbone); Site 1: BamHI, Site 2: BglII;
Rescemu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on Rescemu, go to the web
site 'www.zmtd.lsbate.edu' and follow the links for
'Rescemu.' Grid AA was grown at UC San Diego in 2002. DNA
was extracted from leaf strips, double digested using
BamHI and BglII, and ligated to form circular plasmids.
DH10B cells were transformed and then screened on LB
plates with ampicillin."

FEATURES
source

/lab host="DH10B"
/clone_lib="1119 - Rescuem Mu Grid AA"
/note="Organ: leaf; Vector: Rescuem Mu (engineered from pBluescript backbone); Site 1: BamHI; Site 2: BglII; Rescuem is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on Rescuem, go to the web site 'www.zmbl.iastate.edu' and follow the links for 'Rescuem'. Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

ORIGIN

Query Match 45.4%; Score 23.6; DB 29; Length 90;
Best Local Similarity 76.3%; Pred. No. 1.1e+02;
Matches 29; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTACTATAGGAGACGGCCCAAC 38
19 ATTGTATACGACTACTATAGGCGCTCTGCCGACG 56

RESULT 12
A1353162 95 bp mRNA linear EST 04-JAN-1999
LOCUS zeh0113.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 95)
Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
Liew, C.C.
Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: clliew@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAGCTCGAATTAACCTCTACTAAGG 3'
BACKWARD: 5' CCAGTGAATGTATACGACTACTATAGGCG 3'
Seq primer: 5' GAAATTAACCTCTACTAAGG 3'.
Location/Qualifiers
1..95
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/def_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: lambda ZAP Express; Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

FEATURES

SOURCE

1..95
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/def_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: lambda ZAP Express; Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."

ORIGIN

Query Match

45.4%; Score 23.6; DB 9; Length 95;

Best Local Similarity 69.6%; Pred. No. 1.1e+02;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 TTATATACGACTACTATAGGAGACGGCCCACTGCTAGGA 48
95 TGTATATACGACTACTATAGGCGAATGGGTACTACTGCTGTA 50

RESULT 13
A1353583 95 bp mRNA linear EST 04-JAN-1999
LOCUS zeh0701.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Danio rerio (zebrafish)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 95)
Ton, C., Mably, J.D., Dempsey, A.A., Hwang, D.M., Fishman, M.C. and
Liew, C.C.
Identification and Characterization of Expressed Sequence Tags from
an Embryonic Zebrafish Heart cDNA Library
Unpublished (1999)
Contact: Liew CC
Brigham and Women's Hospital
Harvard Medical School
75 Francis St. Boston, MA 02115, USA
Tel: 6177328915
Fax: 6179750995
Email: clliew@rics.bwh.harvard.edu
PCR Primers
FORWARD: 5' GCCAGCTCGAATTAACCTCTACTAAGG 3'
BACKWARD: 5' CCAGTGAATGTATACGACTACTATAGGCG 3'
Seq primer: 5' GAAATTAACCTCTACTAAGG 3'.
Location/Qualifiers
1..95
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/def_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: lambda ZAP Express; Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."

FEATURES

SOURCE

1..95
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/def_stage="embryonic day 3 post-fertilization"
/lab_host="E.coli XL1-Blue mrf"
/clone_lib="Zebrafish Embryonic Heart cDNA Library"
/note="Organ: heart; Vector: lambda ZAP Express; Site 1:
EcoRI; Site 2: XhoI; mRNA was purified from embryonic
zebrafish hearts (3 day post-fertilization). cDNA was
synthesized using a XhoI-Oligo dT adaptor-primer. EcoRI
adaptors were ligated, followed by digestion with XhoI,
for directional cloning into pre-digested lambda ZAP
Express vector."

ORIGIN

Query Match 45.4%; Score 23.6; DB 9; Length 95;
Best Local Similarity 69.6%; Pred. No. 1.1e+02;
Matches 32; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

Qy 3 TTATATACGACTACTATAGGAGACGGCCCACTGCTAGGA 48
95 TGTATATACGACTACTATAGGCGAATGGGTACTACTGCTGTA 50

RESULT 14
A1617314 96 bp mRNA linear EST 21-APR-1999
LOCUS zehm1391.seq.F Zebrafish Embryonic Heart cDNA Library Danio rerio
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
Danio rerio (zebrafish)

THIS PAGE BLANK (over)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:28:53 ; Search time 81.7143 Seconds

(without alignments)
353.151 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52
Sequence: 1 aatttaatacgaactcactat.....gccaaactgctaggatttc 52

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 27747546 residues

Total number of hits satisfying chosen parameters: 939290

Minimum DB seq length: 0
Maximum DB seq length: 100

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

- 1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
- 3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	36.4	70.0	50	4	US-09-611-627-8 Sequence 8, Appli
2	36.4	70.0	51	4	US-09-611-627-26 Sequence 26, Appli
3	36	69.2	54	4	US-09-168-947-2 Sequence 2, Appli
4	31.8	61.2	52	4	US-09-944-036-7 Sequence 7, Appli
5	31.4	60.4	49	4	US-09-493-491-35 Sequence 35, Appli
6	31.4	60.4	49	4	US-09-493-491A-38 Sequence 38, Appli
7	30.4	58.5	52	4	US-09-168-947-15 Sequence 15, Appli
8	30.2	58.1	50	4	US-09-944-036-5 Sequence 5, Appli
9	30.2	58.1	53	4	US-09-944-036-37 Sequence 37, Appli
10	29.8	57.3	48	4	US-09-040-220D-7 Sequence 7, Appli
11	29.8	57.3	48	4	US-09-265-686-7 Sequence 7, Appli
12	29.8	57.3	48	4	US-09-723-749-7 Sequence 7, Appli
13	29.6	56.9	47	1	US-08-162-836-10 Sequence 10, Appli
14	29.6	56.9	47	1	US-08-345-861-6 Sequence 6, Appli
15	29.6	56.9	47	2	US-08-479-105A-6 Sequence 6, Appli
16	29.6	56.9	47	3	US-09-502-966-3 Sequence 3, Appli
17	29.2	56.2	45	4	US-09-168-947-39 Sequence 39, Appli
18	28.8	55.4	48	4	US-09-611-627-24 Sequence 24, Appli
19	28.8	55.4	49	4	US-09-611-627-28 Sequence 28, Appli
20	28.8	55.4	50	2	US-08-448-267A-1 Sequence 1, Appli
21	28.8	55.4	50	4	US-09-944-036-8 Sequence 8, Appli
22	28.8	55.4	53	1	US-08-384-541-13 Sequence 13, Appli
23	28.8	55.4	53	1	US-08-384-541-14 Sequence 14, Appli
24	28.8	55.4	53	1	US-08-384-541-15 Sequence 15, Appli
25	28.8	55.4	53	1	US-08-384-541-16 Sequence 16, Appli
26	28.2	54.2	46	2	US-08-448-267A-6 Sequence 6, Appli
27	28.2	54.2	51	4	US-09-168-947-25 Sequence 25, Appli

28	28	53.8	32	1	US-08-482-428-14 Sequence 14, Appli
29	28	53.8	32	1	US-08-486-705-14 Sequence 14, Appli
30	28	53.8	32	1	US-09-944-036-3 Sequence 3, Appli
31	28	53.8	35	2	US-08-360-051A-23 Sequence 23, Appli
32	28	53.8	35	4	US-09-202-972-16 Sequence 16, Appli
33	28	53.8	45	1	US-08-692-610-3 Sequence 3, Appli
34	28	53.8	45	1	US-08-683-122-3 Sequence 3, Appli
35	28	53.8	45	1	US-08-421-471-4 Sequence 4, Appli
36	28	53.8	45	1	US-08-683-124-3 Sequence 3, Appli
37	28	53.8	48	1	US-08-162-836-6 Sequence 6, Appli
38	28	53.8	48	4	US-09-710-200-7 Sequence 7, Appli
39	28	53.8	48	4	US-09-975-408-7 Sequence 7, Appli
40	28	53.8	49	1	US-08-384-541-5 Sequence 5, Appli
41	28	53.8	49	1	US-08-384-541-6 Sequence 6, Appli
42	28	53.8	49	1	US-08-384-541-7 Sequence 7, Appli
43	28	53.8	49	1	US-08-384-541-8 Sequence 8, Appli
44	28	53.8	49	1	US-08-692-610-2 Sequence 2, Appli
45	28	53.8	49	1	US-08-683-122-2 Sequence 2, Appli

ALIGNMENTS

```
RESULT 1
US-09-611-627-8
; Sequence 8, Application US/09611627
; Patent No. 6623920
; GENERAL INFORMATION:
; APPLICANT: BEE, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOIK, Dan
; APPLICANT: GINCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/09/611.627
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
; OTHER INFORMATION: for HIV-1 LTR region
US-09-611-627-8
Query Match 70.0%; Score 36.4; DB 4; Length 50;
Best Local Similarity 94.2%; Pred. No. 1.1e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
Oy 1 AATTATATGACTCTATTTAGGAGACGGCGCCACCTCTCTGGATTTC 52
Db 1 AATTATATGACTCTATTTAGGAGACGGCGCCCA--CTGCTAGAGATTTC 50
RESULT 2
US-09-611-627-26
; Sequence 26, Application US/09611627
; Patent No. 6623920
; GENERAL INFORMATION:
; APPLICANT: BEE, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOIK, Dan
; APPLICANT: GINCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/09/611.627
```

```

; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 26
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
US-09-611-627-26
```

```

Query Match
Best Local Similarity 70.0%; Score 36.4; DB 4; Length 51;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```

Qy
1 AATTAAATACGACTCCTATAGGAGACGGCGCCCACTGCTAGGATTT 52
Db
1 AATTAAATACGACTCCTATAGGAGACGGCGCCCA--CTGCTAGGATTT 50
```

```

RESULT 3
US-09-168-947-2
; Sequence 2, Application US/09168947
; Patent No. 6589734
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; APPLICANT: MCDONOUGH, SHERROL H.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/09/168,947
; CURRENT FILING DATE: 1998-10-08
; EARLIER APPLICATION NUMBER: 08/469,067
; EARLIER FILING DATE: 1995-06-06
; EARLIER APPLICATION NUMBER: 07/550,837
; EARLIER FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-2
```

```

Query Match
Best Local Similarity 69.2%; Score 36; DB 4; Length 54;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
Qy
1 AATTAAATACGACTCCTATAGGAGACGGCGCCCACTGCTAGGATTT 52
Db
1 AATTAAATACGACTCCTATAGGAGACGGCGACTTCCGCTGGGACTTT 52
```

```

RESULT 4
US-09-944-036-7
; Sequence 7, Application US/09944036
; Patent No. 6582920
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
```

```

; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 7
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: Promoter
; LOCATION: (1)..(32)
US-09-944-036-7
```

```

Query Match
Best Local Similarity 61.2%; Score 31.8; DB 4; Length 52;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
```

```

Qy
1 AATTAAATACGACTCCTATAGGAGACGGCGCCCACTGCTAGGATTT 51
Db
1 AATTAAATACGACTCCTATAGGAGACCAACCACTCATTCCTGGCTTT 51
```

```

RESULT 5
US-09-493-491-35
; Sequence 35, Application US/09493491
; Patent No. 6391556
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491
; CURRENT FILING DATE: 2000-01-28
; EARLIER APPLICATION NUMBER: 60/117,640 US
; EARLIER FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 35
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-493-491-35
```

```

Query Match
Best Local Similarity 60.4%; Score 31.4; DB 4; Length 49;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy
1 AATTAAATACGACTCCTATAGGAGACGGCGCCCACTG 41
Db
2 AAATTAAATACGACTCCTATAGGAGACTGTGCTGACCTG 42
```

```

RESULT 6
US-09-493-491A-38
; Sequence 38, Application US/09493491A
; Patent No. 6551778
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-02.UT
; CURRENT APPLICATION NUMBER: US/09/493,491A
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
```

PRIOR FILING DATE: 1999-01-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 38
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(28)
US-09-493-491A-38

Query Match 60.4%; Score 31.4; DB 4; Length 49;
Best Local Similarity 85.4%; Pred. No. 0.00016;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACTG 41
Db 2 AAATTATAGCACTACTATAGGAGAGGAGGCTGCTGACTG 42

RESULT 7
US-09-168-947-15
Sequence 15, Application US/09168947
Patent No. 6589734
GENERAL INFORMATION:
APPLICANT: KACIAN, DANIEL L.
APPLICANT: FULTZ, TIMOTHY J.
APPLICANT: MCDONOUGH, SHERROL H.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/09/168,947
CURRENT FILING DATE: 1998-10-08
EARLIER APPLICATION NUMBER: 08/469,067
EARLIER FILING DATE: 1995-06-06
EARLIER APPLICATION NUMBER: 07/550,837
EARLIER FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized nucleic acid molecule
US-09-168-947-15

Query Match 58.5%; Score 30.4; DB 4; Length 52;
Best Local Similarity 85.0%; Pred. No. 0.00043;
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACT 40
Db 1 AATTATAGCACTACTATAGGAGAGGAGGCTGCTCTT 40

RESULT 8
US-09-944-036-5
Sequence 5, Application US/09944036
Patent No. 6582920
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036

CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Gag target sequence
NAME/KEY: Promoter
LOCATION: (1)..(29)
US-09-944-036-5

Query Match 58.1%; Score 30.2; DB 4; Length 50;
Best Local Similarity 91.4%; Pred. No. 0.00052;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCGC 35
Db 3 AATTATAGCACTACTATAGGAGAGGAGGCTGCTC 37

RESULT 9
US-09-944-036-37
Sequence 37, Application US/09944036
Patent No. 6582920
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Protease target
NAME/KEY: Promoter
LOCATION: (1)..(33)
US-09-944-036-37

Query Match 58.1%; Score 30.2; DB 4; Length 53;
Best Local Similarity 74.5%; Pred. No. 0.00052;
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 1 AATTATAGCACTACTATAGGAGCGGCGGCAACTG 51
Db 2 AAATTATAGCACTACTATAGGAGCAACAGCCATTCCTGCTTT 52

RESULT 10
US-09-040-220D-7
Sequence 7, Application US/09040220D
Patent No. 6391311
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR

;; TITLE OF INVENTION: ENDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
;; TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
;; FILE REFERENCE: P1122
;; CURRENT APPLICATION NUMBER: US/09/040,220D
;; CURRENT FILING DATE: 1998-03-17
;; NUMBER OF SEQ ID NOS: 8
;; SEQ ID NO 7
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-48
;; OTHER INFORMATION: Sequence is synthesized
;; Patent No. 6391311
US-09-040-220D-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;
Best Local Similarity 82.9%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 11
US-09-265-686-7
;; Sequence 7, Application US/09265686
;; Patent No. 6455283
;; GENERAL INFORMATION:
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Kuo, Sophia S.
;; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
;; FILE REFERENCE: P1122P2
;; CURRENT APPLICATION NUMBER: US/09/265,686
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: US 09/040,220
;; PRIOR FILING DATE: 1998-03-17
;; PRIOR APPLICATION NUMBER: US 09/184,216
;; PRIOR FILING DATE: 1998-11-02
;; NUMBER OF SEQ ID NOS: 8
;; SEQ ID NO 7
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Artificial
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-48
;; OTHER INFORMATION: Sequence is synthesized
;; Patent No. 6455283
US-09-265-686-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;
Best Local Similarity 82.9%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 12
US-09-723-749-7
;; Sequence 7, Application US/09723749
;; Patent No. 6620784
;; GENERAL INFORMATION:
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Kuo, Sophia S.
;; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
;; FILE REFERENCE: P1122P2D1
;; CURRENT APPLICATION NUMBER: US/09/723,749

;; CURRENT FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: US 09/265,686
;; PRIOR FILING DATE: 1999-03-10
;; PRIOR APPLICATION NUMBER: US 09/040,220
;; PRIOR FILING DATE: 1998-03-17
;; PRIOR APPLICATION NUMBER: US 09/184,216
;; PRIOR FILING DATE: 1998-11-02
;; NUMBER OF SEQ ID NOS: 8
;; SEQ ID NO 7
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: Artificial
;; LOCATION: 1-48
;; OTHER INFORMATION: Sequence is synthesized
;; Patent No. 6620784
US-09-723-749-7

Query Match 57.3%; Score 29.8; DB 4; Length 48;
Best Local Similarity 82.9%; Pred. No. 0.00076;
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41
Db 3 ATTCTATACGACTCACTATAGGCGCGCGAATCCAACTG 43

RESULT 13
US-08-162-836-10
;; Sequence 10, Application US/08162836
;; Patent No. 5554516
;; GENERAL INFORMATION:
;; APPLICANT: Daniel L. Kacian
;; APPLICANT: Diane L. McAllister
;; APPLICANT: Sherrol H. McDonough
;; APPLICANT: Nani Bhushan Dattagupta
;; TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Lyon & Lyon
;; STREET: 611 West Sixth Street
;; CITY: Los Angeles
;; STATE: California
;; COUNTRY: USA
;; ZIP: 90017
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
;; SOFTWARE: Wordperfect (Version 5.1)
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/162,836
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/07/879,686
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Warburg, Richard J.
;; REGISTRATION NUMBER: 32,327
;; REFERENCE/DOCKET NUMBER:
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (213) 489-1600
;; TELEFAX: (213) 955-0440
;; TELEX: 67-3510
;; INFORMATION FOR SEQ ID NO: 10:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 47
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear

US-08-162-836-10

Query Match 56.9%; Score 29.6; DB 1; Length 47;
Best Local Similarity 79.5%; Pred. No. 0.00092;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44
1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44

RESULT 14
US-08-345-861-6
; Sequence 6, Application US/08345861
; Patent No. 5766849
; GENERAL INFORMATION:

APPLICANT: Sherrol H. McDonough
APPLICANT: Daniel L. Kacian
APPLICANT: Nanibhushan Dattagupta
APPLICANT: Diane L. McAllister
APPLICANT: Philip Hammond
APPLICANT: Thomas B. Ryder
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE AMPLIFICATION
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/345,861
FILING DATE:

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,405
FILING DATE: August 4, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Watburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 197/136
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 552-8400
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 47
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-345-861-6

Query Match 56.9%; Score 29.6; DB 1; Length 47;
Best Local Similarity 79.5%; Pred. No. 0.00092;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44
1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44

RESULT 15
US-08-479-105A-6
; Sequence 6, Application US/08479105A
; Patent No. 5908744
; GENERAL INFORMATION:

APPLICANT: Diane L. McAllister
APPLICANT: Philip Hammond
TITLE OF INVENTION: NUCLEIC ACID SEQUENCE
TITLE OF INVENTION: AMPLIFICATION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: MS DOS (5.0)
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,105A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/345,861
FILING DATE: No. 5908744ember 28, 1994
APPLICATION NUMBER: 07/925,405
FILING DATE: August 4, 1992
APPLICATION NUMBER: 07/855,732
FILING DATE: March 19, 1992
APPLICATION NUMBER: 07/550,837
FILING DATE: July 10, 1990
APPLICATION NUMBER: 07/379,501
FILING DATE: July 11, 1989

ATTORNEY/AGENT INFORMATION:
NAME: Heber, Sheldon O.
REGISTRATION NUMBER: 38,179
REFERENCE/DOCKET NUMBER: 213/067
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 47 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-479-105A-6

Query Match 56.9%; Score 29.6; DB 2; Length 47;
Best Local Similarity 79.5%; Pred. No. 0.00092;
Matches 35; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44
1 AATTATACGACTCACTATAGGAGACGGGCGCAACTCTCTA 44

Search completed: August 31, 2004, 04:43:18
Job time : 82.7143 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 31, 2004, 01:37:23 ; Search time 3789.92 Seconds
(without alignments)
67.525 Million cell updates/sec

Title: US-10-001-407-15

Perfect score: 52

Sequence: 1 aattatatacgaactcactat.....gccaaactgtcaggatttc 52

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3337270 seqs, 2460713050 residues

Total number of hits satisfying chosen parameters: 2018620

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10C_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	52	100.0	52	14	US-10-001-407-15
2	36.4	70.0	50	13	US-10-461-790-100
3	36.4	70.0	50	13	US-10-632-658-8
4	36.4	70.0	50	14	US-10-001-407-17
5	36.4	70.0	51	13	US-10-632-658-26
6	36	69.2	54	15	US-10-244-490-2
7	31.8	61.2	52	9	US-09-944-036-7
8	31.8	61.2	52	16	US-10-425-975-7
9	31.4	60.4	49	15	US-10-273-707-38
10	30.4	58.5	52	15	US-10-244-490-15
11	30.2	58.1	50	9	US-09-944-036-5
12	30.2	58.1	50	16	US-10-425-975-5
13	30.2	58.1	53	9	US-09-944-036-37
14	30.2	58.1	53	16	US-10-425-975-37

15	29.8	57.3	48	15	US-10-178-442-7	Sequence 7, Appl
16	29.6	56.9	52	13	US-10-231-843-9	Sequence 9, Appl
17	29.6	56.9	53	13	US-10-461-790-36	Sequence 36, Appl
18	29.4	56.5	43	13	US-10-461-790-48	Sequence 48, Appl
19	29.4	56.5	47	13	US-10-461-790-39	Sequence 39, Appl
20	29.2	56.2	45	15	US-10-244-490-39	Sequence 2, Appl
21	29.2	56.2	47	15	US-10-245-988-2	Sequence 2, Appl
22	29	55.8	55	13	US-10-461-790-116	Sequence 116, App
23	28.8	55.4	48	13	US-10-632-658-24	Sequence 24, Appl
24	28.8	55.4	49	13	US-10-632-658-28	Sequence 28, Appl
25	28.8	55.4	50	9	US-09-944-036-8	Sequence 8, Appl
26	28.8	55.4	50	16	US-10-425-975-8	Sequence 8, Appl
27	28.6	55.0	54	13	US-10-461-790-38	Sequence 38, Appl
28	28.4	54.6	39	15	US-10-077-383-25	Sequence 25, Appl
29	28.4	54.6	45	13	US-10-461-790-49	Sequence 49, Appl
30	28.4	54.6	51	13	US-10-363-852-2	Sequence 2, Appl
31	28.4	54.6	53	15	US-10-231-843-5	Sequence 5, Appl
32	28.4	54.6	57	14	US-10-001-407-18	Sequence 18, Appl
33	28.4	54.6	61	15	US-10-077-383-18	Sequence 18, Appl
34	28.2	54.2	48	14	US-10-006-009-42	Sequence 42, Appl
35	28.2	54.2	51	15	US-10-244-490-25	Sequence 25, Appl
36	28.2	54.2	53	15	US-10-231-843-3	Sequence 3, Appl
37	28.2	54.2	53	15	US-10-231-843-25	Sequence 25, Appl
38	28.2	54.2	56	15	US-10-231-843-7	Sequence 7, Appl
39	28	53.8	32	9	US-09-944-036-3	Sequence 3, Appl
40	28	53.8	32	16	US-10-425-975-3	Sequence 3, Appl
41	28	53.8	35	9	US-09-202-972-16	Sequence 16, Appl
42	28	53.8	45	13	US-10-461-790-47	Sequence 47, Appl
43	28	53.8	48	9	US-09-975-408-7	Sequence 7, Appl
44	28	53.8	48	14	US-10-075-579-7	Sequence 7, Appl
45	28	53.8	49	15	US-10-244-490-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-001-407-15
Sequence 15, Application US/10001407
Publication No. US20020177127A1
GENERAL INFORMATION:
APPLICANT: Yang, Yeasing
APPLICANT: Burrell, Terrie
TITLE OR INVENTION: Compositions and Methods for Detecting
TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
FILE REFERENCE: GP117-03.UT
CURRENT APPLICATION NUMBER: US/10/001.407
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: 60/242,620
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/280,058
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: T7 promoter primer having a promoter sequence
OTHER INFORMATION: appended at the 5' end of an HIV-2 complementary
OTHER INFORMATION: primer sequence
US-10-001-407-15

Query Match 100.0%; Score 52; DB 14; Length 52;
Best Local Similarity 100.0%; Pred. No. 5.5e-13;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATTATATGACCTCATATATGGAGACGGCGCAACCTCTGCGATTTT 52
Db 1 AATTATATGACCTCATATATGGAGACGGCGCAACCTCTGCGATTTT 52

```
RESULT 2
; Sequence 100, Application US/10461790
; Publication No. US20040029111A1
; GENERAL INFORMATION:
; APPLICANT: Linmen, Jeffery M.
; APPLICANT: Kolk, Daniel P.
; APPLICANT: Dockter, Janel M.
; APPLICANT: Getman, Damon K.
; APPLICANT: Yoshimura, Tadaaki
; APPLICANT: Ho-Sing-Ioy, Marcy
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Hepatitis B Virus
; FILE REFERENCE: GP134-02.UT
; CURRENT APPLICATION NUMBER: US/10/461,790
; PRIOR FILING DATE: 2003-06-13
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HIV-specific promoter-primer
US-10-461-790-100
```

```
Query Match          70.0%; Score 36.4; DB 13; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
QY 1 AATTTAATACGACTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
```

```
RESULT 3
; Sequence 8, Application US/10632658
; Publication No. US20040053223A1
; GENERAL INFORMATION:
; APPLICANT: BEB, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOLK, Dan
; APPLICANT: GIACCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/10/632,658
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/611,627
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
US-10-632-658-8
```

```
Query Match          70.0%; Score 36.4; DB 13; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
Db 1 AATTTAATACGACTCACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
```

```
RESULT 4
; Sequence 17, Application US/10001407
; Publication No. US20020177127A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Yeasing
; APPLICANT: Butrell, Terrie
; TITLE OF INVENTION: Compositions and Methods for Detecting
; TITLE OF INVENTION: Human Immunodeficiency Virus 2 (HIV-2)
; FILE REFERENCE: GP117-03.UT
; CURRENT APPLICATION NUMBER: US/10/001,407
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,620
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/280,058
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: T7 promoter primer having a promoter sequence
; OTHER INFORMATION: appended at the 5' end of the sequence given as
US-10-001-407-17
```

```
Query Match          70.0%; Score 36.4; DB 14; Length 50;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
```

```
QY 1 AATTTAATACGACTCACTATAGGAGACGGCGCCCACTGCTAGGATTTT 52
Db 1 AATTTAATACGACTCACTATAGGAGACGGCGCCCA--CTGCTAGGATTTT 50
```

```
RESULT 5
; Sequence 26, Application US/10632658
; Publication No. US20040053223A1
; GENERAL INFORMATION:
; APPLICANT: BEB, Gary G.
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: KOLK, Dan
; APPLICANT: GIACCHETTI, Cristina
; APPLICANT: MCDONOUGH, Sherrol H.
; TITLE OF INVENTION: DETECTION OF HIV-1 BY NUCLEIC ACID AMPLIFICATION
; FILE REFERENCE: GP103-02.UT
; CURRENT APPLICATION NUMBER: US/10/632,658
; PRIOR FILING DATE: 2003-08-01
; PRIOR APPLICATION NUMBER: US/09/611,627
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 60/143,072
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amplification oligomer with 5' promoter sequence,
US-10-632-658-26
```

```
Query Match          70.0%; Score 36.4; DB 13; Length 51;
Best Local Similarity 94.2%; Pred. No. 4.7e-06;
```

Matches 49; Conservative 0; Mismatches 1; Indels 2; Gaps 1;

Qy 1 AATTATACGACTCATTATAGGAGACGGCGCCCAACTCTGATTTT 52
Db 1 AATTATACGACTCATTATAGGAGACGGCGCCA--CTGCTAGAGATTTT 50

RESULT 6

US-10-244-490-2
; Sequence 2, Application US/10244490
; Publication No. US20030152916A1
; GENERAL INFORMATION:
; APPLICANT: KACIAN, DANIEL L.
; APPLICANT: FULTZ, TIMOTHY J.
; TITLE OF INVENTION: DETECTION OF HIV
; FILE REFERENCE: 218/130
; CURRENT APPLICATION NUMBER: US/10/244,490
; CURRENT FILING DATE: 2002-09-16
; PRIOR APPLICATION NUMBER: US/09/168,947
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 08/469,067
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 07/550,837
; PRIOR FILING DATE: 1990-07-10
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 54
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthesized nucleic acid molecule
US-10-244-490-2

Query Match 69.2%; Score 36; DB 15; Length 54;
Best Local Similarity 80.8%; Pred. No. 7.2e-06;
Matches 42; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCATTATAGGAGACGGCGCCCAACTCTGATTTT 52
Db 1 AATTATACGACTCATTATAGGAGACGGCGCACTTCCCTGGGACTTT 52

RESULT 7

US-09-944-036-7
; Sequence 7, Application US/09944036
; Patent No. US20020055095A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/09/944,036
; CURRENT FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(32)

US-09-944-036-7

Query Match 61.2%; Score 31.8; DB 9; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.00053;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCATTATAGGAGACGGCGCCCAACTCTGATTTT 51
Db 1 AATTATACGACTCATTATAGGAGACGACGACATCCATTCCTGCTTT 51

RESULT 8

US-10-425-975-7
; Sequence 7, Application US/10425975
; Publication No. US20030228574A1
; GENERAL INFORMATION:
; APPLICANT: YANG, Yeasing Y.
; APPLICANT: BRENTANO, Steven T.
; APPLICANT: BABOLA, Odile
; APPLICANT: TRAN, Nathalie
; APPLICANT: VERNET, Guy
; TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
; FILE REFERENCE: GP114-02.UT
; CURRENT APPLICATION NUMBER: US/10/425,975
; CURRENT FILING DATE: 2003-04-28
; PRIOR APPLICATION NUMBER: US/09/944,036
; PRIOR FILING DATE: 2001-08-31
; PRIOR APPLICATION NUMBER: US 60/229,790
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Oligonucleotide primer for Protease target
; NAME/KEY: promoter
; LOCATION: (1)..(32)
US-10-425-975-7

Query Match 61.2%; Score 31.8; DB 16; Length 52;
Best Local Similarity 76.5%; Pred. No. 0.00053;
Matches 39; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 AATTATACGACTCATTATAGGAGACGGCGCCCAACTCTGATTTT 51
Db 1 AATTATACGACTCATTATAGGAGACGACGACATCCATTCCTGCTTT 51

RESULT 9

US-10-273-707-38
; Sequence 38, Application US/10273707
; Publication No. US2003010448A1
; GENERAL INFORMATION:
; APPLICANT: HARVEY, Richard, C.
; APPLICANT: CLARK, JR., Thomas, J.
; TITLE OF INVENTION: NUCLEIC ACID SEQUENCES FOR DETECTING GENETIC MARKERS
; FILE REFERENCE: GP097-03.DV1
; CURRENT APPLICATION NUMBER: US/10/273,707
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: 09/493,491
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/117,640 US
; PRIOR FILING DATE: 1999-01-28
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38

LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
FEATURE:
NAME/KEY: Promoter
LOCATION: (1) ... (28)
US-10-273-707-38

Query Match
Best Local Similarity 60.4%; Score 31.4; DB 15; Length 49;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACTG 41
DB 2 AATTATACGACTCACTATAGGAGCGGCGCTGCTGACCTG 42

RESULT 10
US-10-244-490-15
Sequence 15, Application US/10244490
Publication No. US20030152916A1
GENERAL INFORMATION:
APPLICANT: KACIAN, DANIEL L.
APPLICANT: PUTZ, TIMOTHY J.
TITLE OF INVENTION: DETECTION OF HIV
FILE REFERENCE: 218/130
CURRENT APPLICATION NUMBER: US/10/244,490
PRIOR FILING DATE: 2002-09-16
PRIOR APPLICATION NUMBER: US/09/168,947
PRIOR FILING DATE: 1998-10-08
PRIOR APPLICATION NUMBER: 08/469,067
PRIOR FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: 07/550,837
PRIOR FILING DATE: 1990-07-10
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 52
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthesized nucleic acid molecule
US-10-244-490-15

Query Match
Best Local Similarity 58.5%; Score 30.4; DB 15; Length 52;
Matches 34; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCCCAACT 40
DB 1 AATTATACGACTCACTATAGGAGCGGCGCTGCTT 40

RESULT 11
US-09-944-036-5
Sequence 5, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790

PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
NAME/KEY: Promoter
LOCATION: (1) ... (29)
US-09-944-036-5

Query Match
Best Local Similarity 58.1%; Score 30.2; DB 9; Length 50;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCC 35
DB 3 AATTATACGACTCACTATAGGAGAGTGGCTCC 37

RESULT 12
US-10-425-975-5
Sequence 5, Application US/10425975
Publication No. US20030228574A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
FILE REFERENCE: GP114-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
NAME/KEY: Promoter
LOCATION: (1) ... (29)
US-10-425-975-5

Query Match
Best Local Similarity 58.1%; Score 30.2; DB 16; Length 50;
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 AATTATACGACTCACTATAGGAGCGGCGCC 35
DB 3 AATTATACGACTCACTATAGGAGAGTGGCTCC 37

RESULT 13
US-09-944-036-37
Sequence 37, Application US/09944036
Patent No. US20020055095A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile

APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP14-02.UT
CURRENT APPLICATION NUMBER: US/09/944,036
CURRENT FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Protease target
NAME/KEY: Promoter
LOCATION: (1)..(33)
US-09-944-036-37

Query Match 58.1%; Score 30.2; DB 9; Length 53;
Best Local Similarity 74.5%; Pred. No. 0.0027;
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTGCTAGGATTT 51
DB 2 AAATTAAATACGACTACTATATAGGAGACACAGCCATTCATTCCTGGCTTT 52

RESULT 14
US-10-425-975-37
Sequence 37, Application US/10425975
Publication No. US20030228574A1
GENERAL INFORMATION:
APPLICANT: YANG, Yeasing Y.
APPLICANT: BRENTANO, Steven T.
APPLICANT: BABOLA, Odile
APPLICANT: TRAN, Nathalie
APPLICANT: VERNET, Guy
TITLE OF INVENTION: AMPLIFICATION OF HIV-1 SEQUENCES FOR DETECTION OF
TITLE OF INVENTION: SEQUENCES ASSOCIATED WITH DRUG-RESISTANCE MUTATIONS
FILE REFERENCE: GP14-02.UT
CURRENT APPLICATION NUMBER: US/10/425,975
CURRENT FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US/09/944,036
PRIOR FILING DATE: 2001-08-31
PRIOR APPLICATION NUMBER: US 60/229,790
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 37
LENGTH: 53
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
OTHER INFORMATION: Oligonucleotide primer for Protease target
OTHER INFORMATION: Sequence
FEATURE:
NAME/KEY: Promoter
LOCATION: (1)..(33)
US-10-425-975-37

Query Match 58.1%; Score 30.2; DB 16; Length 53;
Best Local Similarity 74.5%; Pred. No. 0.0027;
Matches 38; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTGCTAGGATTT 51
DB 2 AAATTAAATACGACTACTATATAGGAGACACAGCCATTCATTCCTGGCTTT 52

RESULT 15
US-10-178-442-7
Sequence 7, Application US/10178442
Publication No. US20030113870A1
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMP1
FILE REFERENCE: 11669.112USD2
CURRENT APPLICATION NUMBER: US/10/178,442
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: US 09/265,686
PRIOR FILING DATE: 1999-03-10
PRIOR APPLICATION NUMBER: US 09/194,216
PRIOR FILING DATE: 1998-11-02
PRIOR APPLICATION NUMBER: US 09/040,220
PRIOR FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 48
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Sequence is synthesized
US-10-178-442-7

Query Match 57.3%; Score 29.8; DB 15; Length 48;
Best Local Similarity 82.9%; Pred. No. 0.004;
Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 1 AATTAAATACGACTACTATATAGGAGACGGGCGCAACTG 41
DB 3 ATTCTAAATACGACTACTATATAGGAGCGGCGGAATCAACTG 43

Search completed: August 31, 2004, 06:17:10
Job time : 3797.92 secs

THIS PAGE ON FILE